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Scientific and Technical Information Center

CRFE

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10-12-06
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/604926
Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Bio Informatically

Inventors (please provide full names): Bentwich et al

Earliest Priority Date: 8/27/03

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No. 1931

limit to 120 NTS.

Seq ID No: 4539

Size limit to 30 NTS.

1931-61NA
4539-19NA

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GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:31:43 ; Search time 2388 Seconds
(without alignments)
1428.425 Million cell updates/sec

Title: US-10-604-926A-1931
Perfect score: 61
Sequence: 1 agctgcctctctctctcc.....ggagagagggtggtgct 61

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues
Total number of hits satisfying chosen parameters: 1484138

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsl1:*
12: gb_gsl2:*
13: gb_gsl3:*
14: gb_gsl4:*

Result No.	Score	Query Match	Length	ID	Description
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2	43.4	71.1	83	AW009266	AW009266 ws80a06.x
3	27.6	45.2	77	DN374929	DN374929 LIB38529
4	25.6	42.0	103	AA731471	AA731471 nz98f08.5
5	24.4	40.0	82	CW33527	CW33527 104_835.1
6	24.2	40.0	84	CW335786	CW335786 104_834.1
7	24.2	39.7	70	DJ329889	DJ329889 109848604
8	23.6	38.7	69	CW130949	CW130949 104_513.1
9	23.6	38.7	78	CW189398	CW189398 104_610.1
10	23.6	38.7	78	CW189398	CW189398 104_610.1
11	23.6	38.7	82	CW33527	CW33527 104_835.1
12	23.4	38.4	91	BH415834	BH415834 1007045A0
13	23.4	38.4	119	BP112776	BP112776 BP112776
14	23.2	38.0	55	DN373872	DN373872 LIB38528
15	23.2	38.0	68	CR147982	CR147982 Forward's
16	23	37.7	115	AI858529	AI858529 w139h03.x
17	23	37.7	120	BE082457	BE082457 RC5-BT063
18	22.8	37.4	73	AI718969	AI718969 as50f01.x
19	22.8	37.4	98	CF197798	CF197798 maj40b02.

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20	22.8	37.4	111	13	CW189218	CW189218 104_610.1
21	22.6	37.0	112	9	DN440660	DN440660 LIB5337-0
22	22.6	37.0	114	2	BF832254	BF832254 PM3-HT092
23	22.6	37.0	118	1	AI589396	AI589396 tr61h10.x
24	22.4	36.7	99	10	F24424	F24424 HSPD10720 H
25	22.4	36.7	117	12	CG566740	CG566740 OST192605
26	22.2	36.4	76	12	CG668667	CG668667 OST458079
27	22.2	36.4	98	13	CL279855	CL279855 Ggal_142c
28	22.2	36.4	107	8	CO529989	CO529989 3530_1.19
29	22.2	36.4	113	7	AW028147	AW028147 wv26f08.x
30	22.2	36.4	115	5	CD696564	CD696564 EST13087
31	22.2	36.4	119	1	AI824210	AI824210 wj36b05.x
32	22.2	36.4	119	14	CR001418	CR001418 Forward's
33	22	36.1	70	14	DX107181	DX107181 644_2_141
34	22	36.1	70	14	DX107181	DX107181 644_2_141
35	22	36.1	72	14	CR194047	CR194047 Reverse s
36	22	36.1	89	14	CR037539	CR037539 Reverse s
37	22	36.1	94	8	CO887582	CO887582 BovGen.15
38	21.8	35.7	83	11	AZ639232	AZ639232 IM0499M06
39	21.8	35.7	110	5	CI299381	CI299381 CI299381
40	21.8	35.7	117	7	BE487605	BE487605 176447 BA
41	21.8	35.7	118	1	AA646954	AA646954 vt38d09.r
42	21.8	35.7	120	5	CI297065	CI297065 CI297065
43	21.6	35.4	101	5	CD945340	CD945340 RDX_27 Ge
44	21.6	35.4	101	8	CO824350	CO824350 LM_GB5_00
45	21.6	35.4	112	3	BU754334	BU754334 UI-1-BB1p

ALIGNMENTS

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LOCUS HSPD10720 HM3 Homo sapiens cDNA clone s400009E12, mRNA sequence.
DEFINITION F24424 99 bp mRNA linear EST 13-MAY-1999
ACCESSION F24424
VERSION F24424.1 GI:4810050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 99)
AUTHORS Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
TITLE Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
JOURNAL Genome Res. 6 (1), 35-42 (1996)
PUBMED 8681137
COMMENT Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://group.bio.unipd.it.

FEATURES

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="s400009E12"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/clone_lib="HM3"
/note="Vector: pcDNAII (Invitrogen); Site 1: BscXI; Site 2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer
(5'-biotin-AACCGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The ds cDNA was sonicated and size-selected in the range.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1783 Std Error: 0.00
Seq primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 92.
Location/Qualifiers

FEATURES

source

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/lab_host="DH10B"
/clone_lib="NCI CGAP GCBI"
/note="Vector: pTT3D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IGD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-NGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTITTTTTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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ORIGIN

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Best Local Similarity 66.1%; Pred. No. 2.9e+03;
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RESULT 5

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LOCUS 104_835_11483640_148_36099_082 Sorghum methylation filtered library
DEFINITION (LibID: 104) Sorghum bicolor genomic clone 11483640, genomic survey
sequence.
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ACCESSION CW336527

VERSION CW336527.1 GI:55052715

KEYWORDS GSS.

SOURCE Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McWenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and Martienssen,R.A.

Sorghum genome sequencing by methylation filtration

PLOS Biol. 3 (1), e13 (2005)

PUBMED 15660154

COMMENT

Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 835 row: o column: 24

Seq primer: SWfor Forward

Class: methylation filtered

High quality sequence stop: 82.

Location/Qualifiers

1..82

FEATURES

source

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ORIGIN

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Best Local Similarity 63.8%; Pred. No. 6.6e+03;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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RESULT 6

CW335786

LOCUS

DEFINITION

104_834_11483234_116_36083_001 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11483234, genomic survey

sequence.

ACCESSION CW335786

VERSION CW335786.1 GI:55051974

KEYWORDS GSS.

SOURCE Sorghum bicolor (sorghum)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS

Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McWenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddalooh,J.A. and Martienssen,R.A.

Sorghum genome sequencing by methylation filtration

PLOS Biol. 3 (1), e13 (2005)

PUBMED 15660154

COMMENT

Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 834 row: o column: 02

Seq primer: T3 Reverse

Class: methylation filtered

High quality sequence stop: 84.

Location/Qualifiers

1..84

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ORIGIN

source


```
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
FEATURES
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ORIGIN
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Db 23 CCCCCCCCCCCCCCCCCCCCCCGCGCGCGGGGGGGGGGGGGGG 76
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RESULT 10
CW189398/c
LOCUS
DEFINITION
    104 610 11173943 148 37098 086 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11173943, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    Sorghum bicolor (sorghum)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 78)
AUTHORS
    Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McWenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelloh, J.A. and Martienssen, R.A.
TITLE
    Sorghum genome sequencing by methylation filtration
JOURNAL
PUBMED
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
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ORIGIN
    Query Match      38.7%; Score 23.6; DB 13; Length 78;
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RESULT 10
CW189398/c
LOCUS
DEFINITION
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 78)
AUTHORS
    Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McWenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelloh, J.A. and Martienssen, R.A.
TITLE
    Sorghum genome sequencing by methylation filtration
JOURNAL
PUBMED
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 610 row: k column: 23
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 78.
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ORIGIN
    Query Match      38.7%; Score 23.6; DB 13; Length 78;
    Best Local Similarity 64.8%; Pred. No. 1.2e+04;
    Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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RESULT 11
CW336527/c
LOCUS
DEFINITION
    104 835 11483640 148 36099 082 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11483640, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    Sorghum bicolor (sorghum)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
    1 (bases 1 to 82)
AUTHORS
    Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McWenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelloh, J.A. and Martienssen, R.A.
TITLE
    Sorghum genome sequencing by methylation filtration
JOURNAL
PUBMED
    PLoS Biol. 3 (1), e13 (2005)
15660154
COMMENT
Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 835 row: o column: 24
Seq primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 82.
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ORIGIN
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Query Match      38.7%; Score 23.6; DB 13; Length 82;
Best Local Similarity 64.8%; Pred. No. 1.2e+04;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGGTGGGTG 59
Db 73 CGCGCCCCCCCCCCCCCCCCCCCCCGCGGGGGGGGGGGGGGGGGGG 20

RESULT 12
BH415834/c
LOCUS
DEFINITION 1007045A05.x1 1007 - RescueMu Grid H Zea mays genomic, genomic
survey sequence.
ACCESSION BH415834
VERSION BH415834.1 GI:17597044
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Walbot.V.
AUTHORS Zea mays
JOURNAL Zea mays
COMMENT Zea mays

Maize genomic sequences found using engineered RescueMu transposon
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1007045 column: 12
Class: transposon-tagged.
Location/Qualifiers
1..91
/organism="Zea mays"
/mol_type="genomic DNA"
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/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
was extracted from leaf punches, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match      38.4%; Score 23.4; DB 11; Length 91;
Best Local Similarity 73.2%; Pred. No. 1.3e+04;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 AGCTGCCCTCTCTTCTCCCTCACACTACAGCCCTGGTG 41
Db 44 ATCGACCTCTCTTCTCCCTTCCCTTCCACACAGCCCTAGCTAG 4

RESULT 13
BH112776
LOCUS
DEFINITION BP112776 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
ORCS13554 5', mRNA sequence.

Query Match      38.4%; Score 23.4; DB 3; Length 119;
Best Local Similarity 64.7%; Pred. No. 1.4e+04;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 11 CTCTTCTCCCTCACACTACAGCCCTGTGGGGAGAGGGGTGGTCT 61
Db 69 CTCTCNGCCACTTCCCTCCAGCCCTGTGTAGAGTCCAGTGGTGGT 119

RESULT 14
DN373872
LOCUS
DEFINITION DN373872_002_F03_T7_1 LIB38528 Canis familiaris cDNA clone
LIB38528_002_F03, mRNA sequence.
ACCESSION DN373872
VERSION DN373872.1 GI:60555092
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Chordata; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 55)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
Location/Qualifiers
1..55
/organism="Canis familiaris"

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ACCESSION BP112776
VERSION BP112776.1 GI:28315066
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 119)
AUTHORS Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,
Takahashi,T., Inai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,
Suzuki,Y., Tsujimoto,G., Izaika,Y., Todoroki,J. and Hashizume,K.
TITLE Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)
PUBMED 12658628
COMMENT Contact: Goroh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-2476
Fax: 81-3-3149-1252
Email: gtsujimoto@mch.go.jp
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agrobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
and Technology.
Location/Qualifiers
1..119
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/db_xref="taxon:9913"
/clone="ORCS13554"
/tissue_type="mixture of uterus and placenta"
/dev_stage="adult"
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Query Match      38.4%; Score 23.4; DB 3; Length 119;
Best Local Similarity 64.7%; Pred. No. 1.4e+04;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 11 CTCTTCTCCCTCACACTACAGCCCTGTGGGGAGAGGGGTGGTCT 61
Db 69 CTCTCNGCCACTTCCCTCCAGCCCTGTGTAGAGTCCAGTGGTGGT 119

RESULT 14
DN373872
LOCUS
DEFINITION DN373872_002_F03_T7_1 LIB38528 Canis familiaris cDNA clone
LIB38528_002_F03, mRNA sequence.
ACCESSION DN373872
VERSION DN373872.1 GI:60555092
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Chordata; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 55)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
Location/Qualifiers
1..55
/organism="Canis familiaris"

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Job time : 2392 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:29:31 ; Search time 2138 Seconds

(without alignments)
1824.505 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61

Sequence: 1 agctgcctctctctctctcc.....gggagagggggtggtgct 61

Scoring table: IDENTITY_NUC

Gapop_10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2862434

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb_hcg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	25.4	41.6	60	2	A62989 Sequence 1
C 2	23.6	38.7	64	2	BD226837 High thro
C 3	23.6	38.7	64	2	BD226837 High thro
C 4	23.2	38.0	100	5	HUMSYNLE08
C 5	22.8	37.4	70	2	AR012477 Sequence
C 6	22.8	37.4	70	2	AR020305 Sequence
C 7	22.8	37.4	70	2	AR109326 Sequence
C 8	22.8	37.4	70	2	AR368517 Sequence
C 9	22.8	37.4	70	2	I82651 Sequence 92
C 10	22.8	37.4	70	2	AR391709 Sequence
C 11	22.6	37.0	101	4	M14383 N.crassa mi
C 12	22	36.1	66	2	AR072451 Sequence
C 13	22	36.1	66	2	I26562 Sequence 25
C 14	21.4	35.1	100	2	AX989306 Sequence
C 15	21.4	35.1	100	2	AX989307 Sequence
C 16	21.2	34.8	75	2	AR125930 Sequence
C 17	21.2	34.8	75	2	I24297 Sequence 84
C 18	20.8	34.1	100	2	AX989958 Sequence

19	20.8	34.1	100	2	AX989959	Sequence
20	20.6	33.8	90	4	AY947208	Oryza sat
21	20.6	33.8	91	15	FRA23RRNAB	M85113 Frankia sp.
C 22	20.6	33.8	119	7	G32415	G32415 A009C21 Hum
23	20.4	33.4	52	4	D0358817	D0358817 Viola sp.
24	20.4	33.4	60	2	A62989	Sequence 1
25	20.4	33.4	81	4	AY947209	AY947209 Oryza sat
C 26	20.2	33.1	112	5	AY878245	AY878245 Homo sapi
27	20	32.8	66	8	SYN1SGAL	J02555 Rat insulin
28	20	32.8	76	2	AR579029	AR579029 Sequence
29	20	32.8	76	2	AX240936	AX240936 Sequence
30	20	32.8	103	5	S75385810	S75404 collagen ty
31	20	32.8	106	2	CQ148149	CQ148149 Sequence
32	20	32.8	106	2	CQ207925	CQ207925 Sequence
C 33	19.6	32.1	51	2	AX411413	AX411413 Sequence
34	19.6	32.1	119	7	BV194603	BV194603 sqm18161
35	19.6	32.1	120	2	AR248658	AR248658 Sequence
36	19.4	31.8	60	2	CQ539983	CQ539983 Sequence
C 37	19.4	31.8	76	2	AR500694	AR500694 Sequence
C 38	19.4	31.8	76	2	AR515976	AR515976 Sequence
39	19.4	31.8	113	14	AF455673	AF455673 Bos tauru
40	19.2	31.5	50	2	AR681052	AR681052 Sequence
C 41	19.2	31.5	103	2	CQ690519	CQ690519 Sequence
C 42	19	31.1	50	2	AR683151	AR683151 Sequence
43	19	31.1	57	2	AR000467	AR000467 Sequence
C 44	19	31.1	89	2	CQ107196	CQ107196 Sequence
C 45	19	31.1	93	2	BD040459	BD040459 Sequence

ALIGNMENTS

RESULT 1	A62989/c	A62989	Sequence 1 from Patent WO9720068.	60 bp	DNA	linear	PAT 12-MAR-1998
LOCUS	A62989	Sequence 1 from Patent WO9720068.					
DEFINITION	A62989	Sequence 1 from Patent WO9720068.					
ACCESSION	A62989	Sequence 1 from Patent WO9720068.					
VERSION	A62989.1	GI:3716861					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
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Db	60	YYY 8		
RESULT 2				
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LOCUS	BD226837	High through put method for functionally classifying proteins	64 bp	DNA linear PAT 17-JUL-2003
DEFINITION	BD226837	Identified by using genomic approach.		
ACCESSION	BD226837			
VERSION	BD226837.1	GI:33036607		
KEYWORDS	JP 2002514571-A/7.			
SOURCE				
ORGANISM				

[illegible]

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 66)
Prockop, D.J., Ala-Kokko, L., Williams, C.J., Ritvaniemi, P.,
Baldwin, C., Hopkinson, I. and Ahmad, N.Nina,
Primers and methods for detecting mutations in the procollagen II
gene (COL2A1) that indicate a genetic predisposition for a
COL2A1-associated disease
Patent: US 5948611-A 254 07-SEP-1999;
Location/Qualifiers
1. .66
source

[illegible]

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RESULT 15
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LOCUS      AX989307      100 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 770 from Patent EP1260592.
ACCESSION  AX989307
VERSION     AX989307.1  GI:40995653
KEYWORDS
SOURCE
ORGANISM   Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE  1
AUTHORS    Donner, H., Drescher, B., Huber, A. and Weber, J.
TITLE      Biochip
JOURNAL    Patent: EP 1260592-A 770 27-NOV-2002;
            MWG -Biotech AG (DE)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:582"
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ORIGIN
Query Match      35.1%; Score 21.4; DB 2; Length 100;
Best Local Similarity 66.0%; Pred. No. 1.4e+04;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      9 TCCTCTTCCCTCAGCTACTACAGCCCTGTTGGGGGAGAGGGGGTG 55
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Job time : 2141 secs
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GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:27:16 ; Search time 303 Seconds

(without alignments)

1403.654 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61

Sequence: 1 agctgcctctctctctctcc.....gggagagggggtgggtgct 61

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5729524

Minimum DB seq length: 0

Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 12: Geneseqn2004as.*
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- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.8	37.4	70	2 AAT71418	Aat71418 Glioblast
C 2	21.4	35.1	100	8 ACD69499	Ac69499 E. coli K
C 3	21.4	35.1	100	8 ACD69500	Ac69500 E. coli K
4	21.2	34.8	74	14 AED05121	Aed05121 Human IL-
5	21.2	34.8	74	14 AED05124	Aed05124 Human IL-
6	21.2	34.8	75	2 AAO98397	Aa98397 SELEX der
7	21.2	34.8	75	4 AAF70810	Aaf70810 Thrombin
8	20.8	34.1	100	8 ACD70152	Ac70152 E. coli K
9	20.8	34.1	100	8 ACD70151	Ac70151 E. coli K
10	20.2	33.1	116	8 ABX41062	Abx41062 Bovine ES
11	20	32.8	76	4 AAS23493	Aas23493 C. albica
12	20	32.8	106	4 ABA51507	Abas1507 Human bre
13	20	32.8	106	4 AAK43614	Aak43614 Human bon
C 14	19.6	32.1	51	6 ABL60621	Ab160621 Nucleotid
C 15	19.6	32.1	51	6 ABK10896	Abk10896 DNA encod
16	19.6	32.1	120	10 ABX85557	Abx85557 Corn ear-
17	19.4	31.8	57	14 AEB98101	Aeb98101 (SP)10 ge
18	19.4	31.8	60	6 ABN36870	Abn36870 Human spl

C 19	19.4	31.8	87	14 AEB98091	Aeb98091 hGH-(SP)1
C 20	19.4	31.8	87	14 AEB98102	Aeb98102 (SP)10 ge
C 21	19.4	31.8	103	14 AEB70564	Aeb70564 Lysyl hyd
22	19.4	31.8	116	12 ACH90116	Ach90116 Human gen
23	19.2	31.5	37	14 AED05189	Aed05189 Human IL-
24	19.2	31.5	50	6 AED00490	Abz00490 Human leu
25	19.2	31.5	61	3 AEA29504	Aea29504 Codon alt
C 26	19.2	31.5	66	2 AAQ12354	Aaq12354 Euoplum-
27	19.2	31.5	115	4 AAK78349	Aak78349 Human imm
C 28	19	31.1	50	6 ABZ02589	Abz02589 Human leu
29	19	31.1	57	2 AAT16237	Aat16237 A. oryzae
C 30	19	31.1	89	4 AAI47369	Aai47369 Probe #16
C 31	19	31.1	93	3 AAC16714	Aac16714 Human sec
C 32	19	31.1	108	12 ADG99660	Adg99660 Kidney di
C 33	19	31.1	118	13 ADR30298	Adr30298 Mouse gen
34	19	31.1	120	3 AAC22952	Aac22952 Human sec
C 35	18.8	30.8	40	2 AAQ22624	Aaq22624 Sense oli
C 36	18.8	30.8	60	6 ABN35863	Abn35863 Human spl
C 37	18.8	30.8	65	6 ABN56704	Abn56704 Mouse spl
C 38	18.8	30.8	73	6 AAS20394	Aas20394 Human VL
C 39	18.8	30.8	73	6 AAS20398	Aas20398 Human VL
C 40	18.8	30.8	80	12 ADM95681	Adm95681 Rat anti
41	18.8	30.8	84	4 AAI26542	Aai26542 Probe #16
42	18.8	30.8	84	4 ABA74773	Abas74773 Human foe
43	18.8	30.8	84	4 AAI55297	Aai55297 Probe #23
44	18.8	30.8	84	4 ABS49046	Abs49046 Human liv
45	18.8	30.8	84	6 ABS22916	Abs22916 Human gen

ALIGNMENTS

RESULT 1

AAT71418/c

ID AAT71418 standard; DNA; 70 BP.

XX AC AAT71418;

XX DT 01-AUG-1997 (first entry)

XX DE Glioblastoma U251 cell line ligand GBI.156.

XX KW Ligand; glioblastoma; brain; tumour; SELEX; in vivo; imaging;

XX KW systematic evolution of ligands by exponential enrichment; cancer;

XX KW drug delivery; cell line; ss.

XX OS Synthetic.

XX PN WO9634875-A1.

XX PD 07-NOV-1996.

XX PF 01-MAY-1996; 96WO-US0006060.

XX PR 03-MAY-1995; 95US-00433585.

XX PR 03-MAY-1995; 95US-00434001.

XX PR 03-MAY-1995; 95US-00434425.

XX PR 03-MAY-1995; 95US-00437667.

XX PA (NEXS-) NEXSTAR PHARM INC.

XX PA (UYRE-) UNIV RES CORP.

XX PI Jensen KB, Chen H, Morris KN, Stephens A, Gold L;

XX PI WPI; 1996-506092/50.

XX PT Identifying nucleic acid ligands for tissues - by contacting candidate
 XX PT mixt. of nucleic acids with tissue and enriching for increased affinity
 XX PT nucleic acids.

XX PS Claim 22; Page 65; 110pp; English.

XX CC The present sequence is a single stranded DNA ligand to the human brain

CC tumour derived, glioblastoma U251 cell line, prepared by systematic
CC evolution of ligands by exponential enrichment (SELEX). A single stranded
CC DNA pool was incubated with U251 cells, and the tighter binding sequences
CC partitioned from the rest of the pool by filtering the reaction through
CC nitrocellulose filters. Twenty rounds of selection were carried out,
CC using a decreasing concentration of U251 cells as the SELEX progressed.
CC Ligands to glioblastoma cell lines can be used in vivo to image
CC glioblastomas, and for the therapeutic localisation of the ligand or
CC other attached therapeutic agents

XX SQ Sequence 70 BP; 10 A; 17 C; 23 G; 20 T; 0 U; 0 Other;

Query Match 37.4%; Score 22.8; DB 2; Length 70;
Best Local Similarity 66.0%; Pred. No. 1.1e+03;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 CTGCGCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52
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RESULT 2

ACD69499/c
ID ACD69499 standard; DNA; 100 BP.

AC ACD69499;

XX 18-SEP-2003 (first entry)

DE E. coli K12 MG1655 biochip probe SEQ ID 769.

XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX Escherichia coli.

PN EP1260592-A1.

XX 27-NOV-2002.

XX 17-MAY-2001; 2001EP-00112179.

XX 17-MAY-2001; 2001EP-00112179.

XX (MWGB-) MWG-BIOTECH AG.

PI Donner H, Drescher B, Huber A, Weber J;

XX WPI; 2003-241155/24.

XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
PT patterns.

PS Claim 3; Page 130; 2004pp; German.

XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally

CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention

XX SQ Sequence 100 BP; 29 A; 26 C; 25 G; 20 T; 0 U; 0 Other;

Query Match 35.1%; Score 21.4; DB 8; Length 100;
Best Local Similarity 66.0%; Pred. No. 3.2e+03;
Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 9 TCCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGGGTG 55
DB 87 TCCTGTTCCTCACTACCCGTTGTGTGATGGCGGACGACGGCGTG 41

RESULT 3

ACD69500/c
ID ACD69500 standard; DNA; 100 BP.

XX ACD69500;

XX 18-SEP-2003 (first entry)

XX E. coli K12 MG1655 biochip probe SEQ ID 770.

XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX Escherichia coli.

XX EP1260592-A1.

XX 27-NOV-2002.

XX 17-MAY-2001; 2001EP-00112179.

XX 17-MAY-2001; 2001EP-00112179.

XX (MWGB-) MWG-BIOTECH AG.

PI Donner H, Drescher B, Huber A, Weber J;

XX WPI; 2003-241155/24.

XX Biochip containing probes complementary with open reading frames in
PT Escherichia coli K12, useful for detecting gene expression and expression
PT patterns.

PS Claim 3; Page 130; 2004pp; German.

XX This invention describes a novel biochip comprising probe spots, each
CC containing many identical probes. The probes are nucleotide sequences of
CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
CC least one includes a segment of at least 20 bases identical with, or
CC complementary to, a segment of an open reading frame (orf) of Escherichia
CC coli K12. The biochip is used for specific detection of gene expression
CC in K12 and for determining the gene expression pattern, e.g. for
CC diagnostic determination of which E. coli strains are present in the gut,
CC and to determine the effects of e.g. growth media on gene expression. The
CC biochip provides as comprehensive as possible detection of the K12
CC genome, with simultaneous analysis of many different genes with a single
CC device, and comparison of gene expression between K12 and its mutants or
CC other E. coli strains in a single experiment. Apart from qualitative and
CC quantitative information about gene expression, it also allows
CC measurements of population densities for the various strains. The use of
CC synthetic oligonucleotides for preparation of probes allows free
CC variation in probe length and ensures high purity (and thus selectivity,
CC reactivity and reproducibility); also synthetic probes are generally
CC shorter than probes prepared by polymerase chain reaction. ACD68731 to
CC ACD81540 represent oligonucleotide probes used with the biochip described
CC in the invention

XX SQ Sequence 100 BP; 28 A; 26 C; 28 G; 18 T; 0 U; 0 Other;

Query Match 35.1%; Score 21.4; DB 8; Length 100;
 Best Local Similarity 66.0%; Pred. No. 3.2e+03;
 Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 9 TCCTCTTCTCCCTCACACTACAGCCCTGGTGGGAGAGGGGGTG 55
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 Db 99 TCCTGTCCCACTCACTACCGTGTGTATGGCGAGCAGGGCGTG 53

RESULT 4
 AED05121
 ID AED05121 standard; RNA; 74 BP.
 XX
 AC AED05121;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE Human IL-23 binding aptamer, SEQ ID No:91.
 XX
 KW aptamer; interleukin-23; cytokine; pharmaceutical; diagnostic;
 KW autoimmune disease; inflammation; cancer; bone resorption; osteoporosis;
 KW insulin dependent diabetes; immunosuppressive; antiinflammatory;
 KW cytostatic; osteopathic; antidiabetic; neuroprotective; antirheumatic;
 KW antiarthritic; antipsoriatic; dermatological; gastrointestinal-gen.;
 KW antiulcer; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..74
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "All purines are deoxy and all pyrimidines are 2'-
 O-methyl"
 XX
 PN WO2005086835-A2.
 XX
 PD 22-SEP-2005.
 XX
 PF 07-MAR-2005; 2005WO-US007666.
 XX
 PR 05-MAR-2004; 2004US-0550962P.
 PR 07-SEP-2004; 2004US-0608046P.
 XX
 PA (ARCH-) ARCHEMIX CORP.
 XX
 PI Cload ST, Diener JL, Ferguson A, Hamaguchi N, Keene SC;
 PI Lagasse HAD, Sawhney P, Thompson K;
 XX
 WPI; 2005-630794/64.
 XX
 PT New aptamer that specifically binds to IL-23 or its variant, useful for
 PT treating, preventing, or ameliorating, e.g. autoimmune disease,
 PT inflammatory disease, cancer, bone resorption in osteoporosis, or Type I
 PT Diabetes.
 XX
 PS Claim 29; SEQ ID NO 91; 305pp; English.
 XX
 CC The invention relates to aptamers that specifically bind to interleukin-
 CC 23 (IL-23) or interleukin-12 (IL-12), or their variants. The aptamers
 CC comprises a nucleotide sequence selected from SEQ ID NOS 13-66, 71-88, 91
 CC -96, 103-118, 124-134, 135-159, 162, 164-172, 176-178, 181-196, and 199-
 CC 314. Also described are: (1) a pharmaceutical composition comprising an
 CC aptamer selected from one cited above, or its salt, and a pharmaceutical
 CC carrier or diluent; (2) a method of treating, preventing, or ameliorating
 CC a disease mediated by IL-23; (3) a method of treating, preventing, or
 CC ameliorating a disease mediated by IL-12; and (4) a diagnostic method
 CC comprising contacting an aptamer above with a composition suspected of
 CC comprising IL-23 or its variant and detecting the presence or absence of
 CC IL-23 or its variant. The aptamers of the invention are useful as in
 CC vitro or in vivo diagnostic agents. They are also useful in the
 CC treatment, prevention, or amelioration of a disease in vivo. The disease
 CC is an autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis,

CC psoriasis, systemic lupus erythematosus, or irritable bowel disease),
 CC inflammatory disease (e.g. Crohn's Disease or ulcerative colitis), cancer
 CC (e.g. colon cancer, lung cancer, or lung metastases), bone resorption in
 CC osteoporosis, or Type I Diabetes. This sequence represents an aptamer of
 CC the invention.
 XX
 SQ Sequence 74 BP; 14 A; 14 C; 32 G; 0 T; 14 U; 0 Other;
 Query Match 34.8%; Score 21.2; DB 14; Length 74;
 Best Local Similarity 64.7%; Pred. No. 3.6e+03;
 Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCCTGGTGGGAGAGGGGGTGGGTGC 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 19 CVACAGCGCGGUGGCGGCAUUGGGUGGAGUC 52

RESULT 5
 AED05124
 ID AED05124 standard; RNA; 74 BP.
 XX
 AC AED05124;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE Human IL-23 binding aptamer, SEQ ID No:94.
 XX
 KW aptamer; interleukin-23; cytokine; pharmaceutical; diagnostic;
 KW autoimmune disease; inflammation; cancer; bone resorption; osteoporosis;
 KW insulin dependent diabetes; immunosuppressive; antiinflammatory;
 KW cytostatic; osteopathic; antidiabetic; neuroprotective; antirheumatic;
 KW antiarthritic; antipsoriatic; dermatological; gastrointestinal-gen.;
 KW antiulcer; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..74
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "All purines are deoxy and all pyrimidines are 2'-
 O-methyl"
 XX
 PN WO2005086835-A2.
 XX
 PD 22-SEP-2005.
 XX
 PF 07-MAR-2005; 2005WO-US007666.
 XX
 PR 05-MAR-2004; 2004US-0550962P.
 PR 07-SEP-2004; 2004US-0608046P.
 XX
 PA (ARCH-) ARCHEMIX CORP.
 XX
 PI Cload ST, Diener JL, Ferguson A, Hamaguchi N, Keene SC;
 PI Lagasse HAD, Sawhney P, Thompson K;
 XX
 WPI; 2005-630794/64.
 XX
 PT New aptamer that specifically binds to IL-23 or its variant, useful for
 PT treating, preventing, or ameliorating, e.g. autoimmune disease,
 PT inflammatory disease, cancer, bone resorption in osteoporosis, or Type I
 PT Diabetes.
 XX
 PS Claim 29; SEQ ID NO 94; 305pp; English.
 XX
 CC The invention relates to aptamers that specifically bind to interleukin-
 CC 23 (IL-23) or interleukin-12 (IL-12), or their variants. The aptamers
 CC comprises a nucleotide sequence selected from SEQ ID NOS 13-66, 71-88, 91
 CC -96, 103-118, 124-134, 135-159, 162, 164-172, 176-178, 181-196, and 199-
 CC 314. Also described are: (1) a pharmaceutical composition comprising an
 CC aptamer selected from one cited above, or its salt, and a pharmaceutical
 CC carrier or diluent; (2) a method of treating, preventing, or ameliorating
 CC a disease mediated by IL-23; (3) a method of treating, preventing, or
 CC ameliorating a disease mediated by IL-12; and (4) a diagnostic method
 CC comprising contacting an aptamer above with a composition suspected of
 CC comprising IL-23 or its variant and detecting the presence or absence of
 CC IL-23 or its variant. The aptamers of the invention are useful as in
 CC vitro or in vivo diagnostic agents. They are also useful in the
 CC treatment, prevention, or amelioration of a disease in vivo. The disease
 CC is an autoimmune disease (e.g. multiple sclerosis, rheumatoid arthritis,


```
Query Match      34.8%; Score 21.2; DB 4; Length 75;
Best Local Similarity 76.5%; Pred. No. 3.6e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 23 CACACTACAGCCTGTGGGGAGAGAGGGGTGG 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15 CATGCTACACCCGTGTAGGGTAGGATGGGGTGG 48

RESULT 8
ACD70152
ID ACD70152 standard; DNA; 100 BP.
XX
AC ACD70152;
XX
DT 18-SEP-2003 (first entry)
XX
DE E. coli K12 MG1655 biochip probe SEQ ID 1422.
XX
KW Biochip: gene expression; gut; diagnostic; detection; probe; ss.
XX
OS Escherichia coli.
XX
FN EPI260592-A1.
XX
PD 27-NOV-2002.
XX
PF 17-MAY-2001; 2001EP-00112179.
XX
PR 17-MAY-2001; 2001EP-00112179.
XX
PA (MWGB-) MWG-BIOTECH AG.
XX
PI Donner H, Drescher B, Huber A, Weber J;
XX
DR WPI; 2003-241155/24.
XX
Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression
patterns.

FS Claim 3; Page 231; 2004pp; German.
XX
This invention describes a novel biochip comprising probe spots, each
containing many identical probes. The probes are nucleotide sequences of
30-80 bases, are prepared ex situ from synthetic oligonucleotides and at
least one includes a segment of at least 20 bases identical with, or
complementary to, a segment of an open reading frame (orf) of Escherichia
coli K12. The biochip is used for specific detection of gene expression
in K12 and for determining the gene expression pattern, e.g. for
diagnostic determination of which E. coli strains are present in the gut,
and to determine the effects of e.g. growth media on gene expression. The
biochip provides as comprehensive as possible detection of the K12
genome, with simultaneous analysis of many different genes with a single
device, and comparison of gene expression between K12 and its mutants or
other E. coli strains in a single experiment. Apart from qualitative and
quantitative information about gene expression, it also allows
measurements of population densities for the various strains. The use of
synthetic oligonucleotides for preparation of probes allows free
variation in probe length and ensures high purity (and thus selectivity,
reactivity and reproducibility); also synthetic probes are generally
shorter than probes prepared by polymerase chain reaction. ACD68731 to
ACD81540 represent oligonucleotide probes used with the biochip described
in the invention

SQ Sequence 100 BP; 23 A; 29 C; 26 G; 22 T; 0 U; 0 Other;
Query Match      34.1%; Score 20.8; DB 8; Length 100;
Best Local Similarity 60.7%; Pred. No. 4.9e+03;
Matches 34; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 AGCTGCCCTCTCTTCTCCCTCCTACACTACAGCCCTGTGGGGAGAGGGGTGG 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 28 AACTGGCCTGCTTTCTCTCTCTGCGCTTCAGGCGTCCGCGAGTGGAGAAATCTGG 83

RESULT 10
ABX41062
```


KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer; ss.
 XX Homo sapiens.
 XX OS
 XX PN WO200157271-A2.
 XX PD
 XX PF 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-496933/54.
 XX PT New spatially-addressable set of single exon nucleic acid probes, useful
 XX PT for measuring gene expression in sample derived from human breast,
 XX PT comprises number of single exon nucleic acid probes.
 XX PS Claim 4; SEQ ID NO 10202; 327pp + Sequence Listing; English.
 XX CC The invention relates to a spatially-addressable set of single exon
 XX CC nucleic acid probes for measuring gene expression in a sample derived
 XX CC from human breast and BT 474 cells. The method involves contacting the
 XX CC probes with a collection of detectably labelled nucleic acids derived
 XX CC from mRNA of human breast, and then measuring the label bound to each
 XX CC probe of the microarray. The probes are useful for verifying the
 XX CC expression of regions of genomic DNA predicted to encode proteins. They
 XX CC are useful for gene discovery, and for determining predisposition and/or
 XX CC prognosing breast disease. Gene expression analysis is useful for
 XX CC assessing the toxicity of chemical agents on cells. The microarray of
 XX CC this invention presents a far greater diversity of probes for measuring
 XX CC gene expression, with far less bias than expressed sequence tag
 XX CC microarrays. The method is suitable for rapid production of functional
 XX CC information from genomic sequence. The present sequence is a single exon
 XX CC nucleic acid probe of the invention. Note: The sequence data for this
 XX CC patent did not form part of the printed specification, but was obtained
 XX CC in electronic format directly from WIPO at
 XX CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 106 BP; 35 A; 24 C; 15 G; 32 T; 0 U; 0 Other;
 Query Match 32.8%; Score 20; DB 4; Length 106;
 Best Local Similarity 65.9%; Pred. NO. 8.8e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 6 CCCTCTCTTCTCCCTCAGCTACAGCCCTGGTGGGAGAG 49
 |||||
 DB 29 CCCTCTCTTCTCTCTCAATTGGAGATGATGAGATGAAG 72
 |||||
 RESULT 13
 AAK43614
 ID AAK43614 standard; DNA; 106 BP.
 XX AC AAK43614;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed single exon probe SEQ ID NO: 18171.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.
 XX OS
 XX PN WO200157276-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000668.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488900/53.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 XX PT gene expression in human bone marrow.
 XX PS Example 4; SEQ ID NO 18171; 658pp + Sequence Listing; English.
 XX CC The present invention provides a number of single exon nucleic acid
 XX CC probes which are derived from genomic sequences expressed in the human
 XX CC bone marrow. They can be used to measure gene expression in bone marrow
 XX CC samples, which may enable the improved diagnosis and treatment of cancers
 XX CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 XX CC the probes of the invention
 XX SQ Sequence 106 BP; 35 A; 24 C; 15 G; 32 T; 0 U; 0 Other;
 Query Match 32.8%; Score 20; DB 4; Length 106;
 Best Local Similarity 65.9%; Pred. NO. 8.8e+03;
 Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 6 CCCTCTCTTCTCCCTCAGCTACAGCCCTGGTGGGAGAG 49
 |||||
 DB 29 CCCTCTCTTCTCTCTCAATTGGAGATGATGAGATGAAG 72
 |||||
 RESULT 14
 ABL60621/c
 ID ABL60621 standard; DNA; 51 BP.
 XX AC ABL60621;
 XX DT 27-AUG-2002 (first entry)
 XX DE Nucleotide fragment from vector pMM106H.
 XX KW Nuclease; tagged protein; protein production; glutathione S transferase;
 KW GST; ds.
 XX OS Synthetic.
 XX PN WO20027327-A2.
 XX PD 04-APR-2002.
 XX PF 17-AUG-2001; 2001WO-GB003693.
 XX PR 17-AUG-2000; 2000GB-00020357.
 XX PR 14-NOV-2000; 2000US-0247995P.
 XX PA (SENS-) SENSE PROTEOMIC LTD.
 XX PI Blackburn JM, Mulder MA, Samaddar M, Kozlowski R;

```
XX WPI: 2002-471270/50.
DR P-PSDB; ABB08039.
XX
XX Producing proteins having full-length, correctly folded domains and
PT marker moiety-tagged N- or C-terminals, by genetically modifying cDNA to
PT encode individual protein having marker moiety fused to N- or C-terminus.
XX
XX Example; Fig 1a; 47pp; English.
PS
XX The invention relates to producing full-length proteins incorporating
XX alpha-S-DNTPs and dNTPs into DNA (I) encoding protein, protecting ends of
CC (I) from nuclease digestion, generating (I) in which set of nested
CC deletions are generated and 5' or 3' untranslated region (UTR) of open
CC reading frame (ORF) are removed, by nuclease digestion, cloning fragments
CC into vector having coding sequence for 5'/3' marker moiety, and
CC expressing proteins. An array comprising proteins prepared by the above
CC method is useful for screening one or more compounds for biological
CC activity; one or more proteins for specific protein-protein interactions
CC or protein-nucleic acid interactions. The array is useful in the rapid
CC screening of a protein, compound or nucleic acid, and also for screening
CC for molecules (preferably, antibodies) which recognize each protein in
CC the array. It is also useful for generating an antibody array. The tagged
CC proteins produced by the methods are useful for analysis of interaction
CC between expressed protein and other proteins, immobilisation on an
CC affinity column/substrate for example to allow the purification by
CC affinity chromatography of, interacting proteins, DNA or chemical
CC compounds; in the immobilization by affinity purification for
CC microarray for identifying DNA binding proteins; or for elucidating the
CC identity of proteins in the proteome, where mass spectrometric analysis
CC of expressed protein components of source library or start material
CC modified by the methods, are performed. The antibody arrays produced
CC using (I) are useful for screening of protein function or abundance. The
CC present sequence represents nucleotide fragment from vector pMW106H
XX
SQ Sequence 51 BP; 19 A; 19 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 32.1%; Score 19.6; DB 6; Length 51;
Best Local Similarity 73.5%; Pred. No. 1.1e+04;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 28 TACAGCCCTGGTGGGAGAGAGGGGGTGGTGCT 61
DB 46 TAGAGCCCTAGTGGTGGTGGTGGTGGTGGT 13
RESULT 15
ID ABK10896/c
AC ABK10896;
XX
XX 21-MAY-2002 (first entry)
XX
XX DNA encoding polyasparagine, hexahistidine fusion peptide (Asn-His tag).
XX
XX Jellyfish; protein array; marker group tag; rapid screening;
KW fusion peptide; ds.
XX
XX Aequorea victoria.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 4..51
FT CDS /tag= a
FT /partial
FT /product= "Polyasparagine hexahistidine fusion peptide"
FT /transl_except= (Pos:37..39, aa:Glu)
FT /note= "This sequence lacks both a start and stop codon"
FT 4..36
FT misc_feature /tag= b
FT
```

```
FT misc_feature /note= "Encodes Asn-His tag"
FT 40..52
FT /*tag= C
FT /note= "Encodes jellyfish green fluorescent protein
(GFP)"
XX
XX WO200157198-A2.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-GB000395.
XX
XX 31-JAN-2000; 2000GB-00002215.
XX
XX 12-APR-2000; 2000US-0196490P.
XX
XX 11-AUG-2000; 2000GB-00019888.
XX
XX (SENS-) SENSE PROTEOMIC LTD.
XX
XX Blackburn JM, Sutherland JD, Samaddar M, Mulder MA, Kozlowski RZ;
XX
XX WPI: 2002-226206/28.
XX
XX P-PSDB; AAU77202.
XX
XX Method for generating a protein array for the rapid screening of a
XX compound, protein or nucleic acid, comprises cloning and expressing
XX protein(s) as full length protein(s), which are tagged with a marker
XX group at either the N- or C-terminal.
XX
XX Example 1; Fig 1a; 47pp; English.
XX
XX The present invention relates to a new method of generating a protein
XX array. The method of the invention involves cloning and expressing one or
XX more proteins as full length proteins, which are each tagged at either
XX the N- or C-terminal with a marker group. The method is useful for
XX providing or generating an array. The array is useful in the rapid
XX screening of a compound, protein or nucleic acid, and in screening for
XX molecules that recognise each protein in the array, where the molecules
XX are preferably antibodies. The present nucleic acid sequence encodes the
XX polyasparagine hexahistidine fusion peptide of the invention. The peptide
XX contains a histidine tag followed by an amber stop codon which is then
XX followed by the gene encoding the green fluorescent protein (GFP) of the
XX jellyfish Aequorea victoria
XX
XX Sequence 51 BP; 19 A; 19 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 32.1%; Score 19.6; DB 6; Length 51;
Best Local Similarity 73.5%; Pred. No. 1.1e+04;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 28 TACAGCCCTGGTGGGAGAGAGGGGGTGGTGCT 61
DB 46 TAGAGCCCTAGTGGTGGTGGTGGTGGTGGT 13
Search completed: October 14, 2006, 19:32:29
Job time : 307 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:32:46 ; Search time 100 Seconds
(without alignments)
1141.376 Million cell updates/sec

Title: US-10-604-926A-1931
Perfect score: 61
Sequence: 1 agctgcctctctctctcc.....gggagaggggtgggtgct 61

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues
Total number of hits satisfying chosen parameters: 1580294

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq: *
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq: *
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq: *
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq: *
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8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq: *
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq: *
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.8	37.4	70	2 US-08-434-001-92	Sequence 92, Appl
C 2	22.8	37.4	70	2 US-08-433-585-92	Sequence 92, Appl
C 3	22.8	37.4	70	2 US-08-434-425-92	Sequence 92, Appl
C 4	22.8	37.4	70	2 US-08-437-667-92	Sequence 92, Appl
C 5	22.8	37.4	70	3 US-08-906-955-92	Sequence 92, Appl
C 6	22.8	37.4	70	3 US-08-945-909-92	Sequence 92, Appl
C 7	22.8	37.4	70	3 US-09-396-002A-92	Sequence 92, Appl
C 8	22.8	37.4	70	3 US-10-077-319-92	Sequence 92, Appl
C 9	22.8	37.4	70	7 PCT-US96-06080-92	Sequence 92, Appl
C 10	22	36.1	66	2 US-07-977-284A-254	Sequence 254, App
C 11	22	36.1	66	2 US-08-256-426B-254	Sequence 254, App
C 12	21.2	34.8	75	3 US-08-219-012-84	Sequence 84, Appl
C 13	21.2	34.8	75	3 US-08-687-421-272	Sequence 272, App
C 14	20	32.8	76	3 US-09-792-024-174	Sequence 174, App
C 15	19.6	32.1	120	3 US-09-313-294A-4017	Sequence 4017, Ap
C 16	19.4	31.8	76	3 US-09-270-767-5654	Sequence 5654, Ap
C 17	19.4	31.8	76	3 US-09-270-767-20936	Sequence 20936, A
C 18	19.2	31.5	50	3 US-10-131-827-481	Sequence 481, App
C 19	19.2	31.5	50	3 US-10-131-831-481	Sequence 481, App
C 20	19	31.1	50	3 US-10-131-827-2580	Sequence 2580, Ap
C 21	19	31.1	50	5 US-10-131-831-2580	Sequence 2580, Ap
C 22	19	31.1	57	2 US-08-596-985-4	Sequence 4, Appl
C 23	19	31.1	93	3 US-09-513-999C-20789	Sequence 20789, A

ALIGNMENTS

RESULT 1
US-08-434-001-92/c
; Sequence 92, Application US/08434001
; Patent No. 5712375
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; NUMBER OF SEQUENCES: 235
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,001
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433

Sequence 27027, A
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 112, App
Sequence 33460, A
Sequence 23, Appl
Sequence 21, Appl
Sequence 32, Appl
Sequence 31, Appl
Patent No. 5200327
Sequence 322, App
Sequence 322, App
Sequence 322, App
Sequence 322, App
Sequence 96, Appl
Sequence 96, Appl
Sequence 96, Appl
Sequence 31, Appl
Sequence 219, App
Sequence 9, Appl
Sequence 34, Appl

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-434-001-92

Query Match 37.4%; Score 22.8; DB 2; Length 70;

Best Local Similarity 66.0%; Pred. No. 1.8e+02;

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCCTCTCTCCCTCCTACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCTCTGGCCCCAAGTCACTACTGCTTAGGAGGCTCACACAGG 2

RESULT 2

US-08-433-585-92/c

; Sequence 92, Application US/08433585

; Patent No. 5763566

; GENERAL INFORMATION:

; APPLICANT: JENSEN, KIRK

; APPLICANT: CHEN, HANG

; APPLICANT: MORRIS, KEVIN

; APPLICANT: STEPHENS, ANDREW

; APPLICANT: GOLD, LARRY

; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY

; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE

; NUMBER OF SEQUENCES: 235

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM: Diskette, 3 1/2 diskette, 1.44 MB

; MEDIUM TYPE: IBM pc compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA: US/08/433,585

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/964,624

; FILING DATE: 21-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX30.4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-433-585-92

Query Match

Best Local Similarity 37.4%; Score 22.8; DB 2; Length 70;

; Sequence 92, Application US/08437667

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCCTCTCTCCCTCCTACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCCTCTGGCCCCAAGTCACTACTGCTTAGGAGGCTCACACAGG 2

RESULT 3

US-08-434-425-92/c

; Sequence 92, Application US/08434425

; Patent No. 5789157

; GENERAL INFORMATION:

; APPLICANT: JENSEN, KIRK

; APPLICANT: CHEN, HANG

; APPLICANT: MOREIS, KEVIN

; APPLICANT: STEPHENS, ANDREW

; APPLICANT: GOLD, LARRY

; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY

; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE

; NUMBER OF SEQUENCES: 235

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM: Diskette, 3 1/2 diskette, 1.44 MB

; MEDIUM TYPE: IBM pc compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA: US/08/434,425

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/964,624

; FILING DATE: 21-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX30.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 92:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 70 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-434-425-92

Query Match

Best Local Similarity 37.4%; Score 22.8; DB 2; Length 70;

; Sequence 92, Application US/08437667

Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 CTGCCCTCCTCTCTCCCTCCTACACTACAGCCCTGGTGGGGAGAGGGG 52

Db 51 CTACCCCTCCTCTGGCCCCAAGTCACTACTGCTTAGGAGGCTCACACAGG 2

RESULT 4

US-08-437-667-92/c

; Sequence 92, Application US/08437667

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,909
FILING DATE:
CLASSIFICATION: 435

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RESULT 7
US-09-396-002A-92/c
; Sequence 92, Application US/09396002A
; Patent No. 6376474
; GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/396,002A
; FILING DATE: 14-Sep-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; APPLICATION NUMBER: 08/906,955
; FILING DATE: 05-AUGUST-1997
; ATTORNEY/AGENT INFORMATION:

```

1 GOLD, LARRY
2
3 TITLE OP INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
4
5 NUMBER OF SEQUENCES: 240
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Swanson & Bratschun, L.L.C.
8 STREET: 1745 Shea Center Drive, Suite 330
9 CITY: Highlands Ranch
10 STATE: Colorado
11 COUNTRY: USA
12 ZIP: 80129
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
16 COMPUTER: IBM pc compatible
17 OPERATING SYSTEM: MS-DOS
18 SOFTWARE: WordPerfect 8.0
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/10/077,319
22 FILING DATE: 14-Feb-2002
23 CLASSIFICATION: -Unknown>
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 09/396,002
27 FILING DATE: 14-Sep-1999
28 APPLICATION NUMBER: 07/714,131
29 FILING DATE: 10-JUNE-1991
30 APPLICATION NUMBER: 08/434,001
31 FILING DATE: 05-MAY-1995
32 APPLICATION NUMBER: 08/906,955
33 FILING DATE: 05-AUGUST-1997
34
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Barry J. Swanson
37 REGISTRATION NUMBER: 33,215
38 REFERENCE/DOCKET NUMBER: NEX30-5/D
39
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (303) 268-0066
42 TELEFAX: (303) 268-0065
43
44 INFORMATION FOR SEQ ID NO: 92:
45
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 70 base pairs
48 TYPE: nucleic acid
49 STRANDEDNESS: single
50 TOPOLOGY: linear
51
52 SEQUENCE DESCRIPTION: SEQ ID NO: 92:

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US-10-077-319-92

Query Match 37.4%; Score 22.8; DB 3; Length 70;
Best Local Similarity 66.0%; Pred. No. 1.8e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTGCGCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGG 52
DB 51 CTACCCCTCTCTGCGCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 9

PCT-US96-06060-92/c
; Sequence 92, Application PC/TUS9606060
; GENERAL INFORMATION:
; APPLICANT: JENSEN, KIRK
; APPLICANT: CHEN, HANG
; APPLICANT: MORRIS, KEVIN
; APPLICANT: STEPHENS, ANDREW
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; TITLE OF INVENTION: EXPONENTIAL ENRICHMENT: TISSUE
; TITLE OF INVENTION: SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06060
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,425
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/437,667
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,585
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30/PCT
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
PCT-US96-06060-92

Query Match 37.4%; Score 22.8; DB 7; Length 70;
Best Local Similarity 66.0%; Pred. No. 1.8e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 CTGCGCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGG 52
DB 51 CTACCCCTCTCTGCGCCCAAGTCACTACTGCTAGGAGGCTCACACAGG 2

RESULT 10

US-07-977-284A-254/c
; Sequence 254, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
; TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,284A
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-07-977-284A-254

Query Match 36.1%; Score 22; DB 2; Length 66;
Best Local Similarity 63.0%; Pred. No. 3.3e+02;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGGTGGTG 59
DB 55 CTCTCTCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2

RESULT 11

US-08-256-426B-254/c

```
; Sequence 254, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Frockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256.426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 254:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-256-426B-254

Query Match 36.1%; Score 22; DB 2; Length 66;
Best Local Similarity 63.0%; Pred. No. 3.3e+02;
Matches 34; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 6 CCCTCTCTTCTCCCTCACACTACAGCCCTGGTGGGGGAGAGGGGGTGG 59
Db 55 CTCCTCTTCTTCTGCCCGGGGGGGGGGGGGGGGGGGGGGGGGGG 2

RESULT 12
US-08-219-012-84
; Sequence 84, Application US/08219012
; Patent No. 5543293
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Diane Tasset
; TITLE OF INVENTION: Ligands of Thrombin
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, Suite #
; STREET: 403
; CITY: Denver

; Sequence 254, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Frockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
; STREET: One liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE: 08-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,005
; FILING DATE: 10-FEBRUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 22-APRIL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/219,012

; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,012
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: none
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-219-012-84

Query Match 34.8%; Score 21.2; DB 2; Length 75;
Best Local Similarity 76.5%; Pred. No. 6.2e+02;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 23 CACACTACAGCCCTGGTGGGGGAGAGGGGGTGG 56
Db 15 CATGCTACACCCGTGGTAGGGTAGGTGGGGTGG 48

RESULT 13
US-08-687-421-272
; Sequence 272, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Tasset, Diane
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 445
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,421
; FILING DATE: 08-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,005
; FILING DATE: 10-FEBRUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 22-APRIL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/219,012
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FILING DATE: 28-MARCH-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/973,333
 FILING DATE: 11-NOVEMBER-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/714,131
 FILING DATE: 10-JUNE-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/536,428
 FILING DATE: 11-JUNE-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEX07/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 272:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 75 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-687-421-272

Query Match 34.8%; Score 21.2; DB 3; Length 75;
 Best Local Similarity 76.5%; Pred. No. 6.2e+02;
 Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 23 CACACTACAGCCCTGGTGGGGAGAAAGGGGGTGG 56
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 CATGCTACACCCGTGGTAGGGTAGGATGGGGGTGG 48

RESULT 14
US-09-792-024-174
; Sequence 174, Application US/09792024

```

: PATENT NO. 6783985
: GENERAL INFORMATION:
: APPLICANT: Roemer, Terry
: APPLICANT: Jiang, Bo
: APPLICANT: Boone, Charles
: APPLICANT: Bussey, Howard
: TITLE OF INVENTION: Gene Disruption Methodologies for Drug
: TITLE OF INVENTION: Targets Discovery
: FILE REFERENCE: 10182-004-999
: CURRENT APPLICATION NUMBER: US/09/792.024
: CURRENT FILING DATE: 2001-02-20
: NUMBER OF SEQ ID NOS: 490
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 174
: LENGTH: 76
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: DNA primer
: US-09-792-024-174

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Query Match	32.8%	Score 20;	DB 3;	Length 76;
Best Local Similarity	61.5%	Pred. No. 1.5e+03;		
Matches 32;	Conservative	0;	Mismatches 20;	Indels 0;
				Gaps 0;

Qy 3 CTGGCCCTCTCTTCTCCCTCCACTACAGCCCTGGTGGGGGGAAGAGGGGGT 54

Dp 23 CTCTCTCTCTCGTCTCCGCCCTCAACCAAGCCCGCTCTAGAACTAGTGGAT 74

RESULT 15
US-09-313-294A-4017
; Sequence 4017, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Laigudi, Raghunath V.

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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:34:24 ; Search time 847 Seconds
(without alignments)
884.942 Million cell updates/sec

Title: US-10-604-926A-1931
Perfect score: 61
Sequence: 1 agctgcctctctctctcc.....gggagaaagggtgggtgct 61

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24482366

Minimum DB seq length: 0
Maximum DB seq length: 120

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	61	11	US-10-310-914A-14543
2	25	41.0	25	15	US-11-121-849-23506
3	24.2	39.7	61	11	US-10-310-914A-14543
4	23.6	38.7	64	6	US-10-057-940-7
5	23.6	38.7	64	6	US-10-057-940-7
6	23	37.7	23	11	US-10-310-914A-148966
7	23	37.7	23	11	US-10-310-914A-148976
8	23	37.7	23	11	US-10-310-914A-1065883
9	23	37.7	23	11	US-10-310-914A-1065889
10	22.8	37.4	70	6	US-10-077-319-92
11	22	36.1	22	11	US-10-310-914A-148933
12	22	36.1	22	11	US-10-310-914A-148939
13	22	36.1	22	11	US-10-310-914A-1065861
14	22	36.1	22	11	US-10-310-914A-1065867
15	22	36.1	23	11	US-10-310-914A-148934
16	21.2	34.8	61	11	US-10-310-914A-3094
17	21.2	34.8	85	11	US-10-310-914A-16745

c 18	21	34.4	21	11	US-10-310-914A-148975	Sequence 148975,
c 19	21	34.4	21	11	US-10-310-914A-1065850	Sequence 1065850,
c 20	21	34.4	21	11	US-10-310-914A-1065888	Sequence 1065888,
c 21	20.8	33.8	110	7	US-10-094-097B-92	Sequence 92, Appl
c 22	20.6	33.8	63	11	US-10-310-914A-15139	Sequence 15139, A
c 23	20.2	33.1	62	11	US-10-310-914A-17901	Sequence 17901, A
c 24	20.2	33.1	116	3	US-09-960-332-6227	Sequence 6227, Ap
c 25	20	32.8	20	11	US-10-310-914A-148986	Sequence 148986,
c 26	20	32.8	20	11	US-10-310-914A-1065897	Sequence 1065897,
c 27	20	32.8	76	10	US-10-882-104-174	Sequence 174, App
c 28	20	32.8	106	3	US-09-864-761-32531	Sequence 32531, A
c 29	19.8	32.5	111	10	US-10-708-204-6052	Sequence 6052, Ap
c 30	19.8	32.5	117	3	US-09-783-590-3277	Sequence 3277, Ap
c 31	19.6	32.1	51	6	US-11-114-334-21	Sequence 21, Appl
c 32	19.6	32.1	51	16	US-11-237-597-21	Sequence 21, Appl
c 33	19.6	32.1	69	11	US-10-310-914A-20353	Sequence 20353, A
c 34	19.6	32.1	73	11	US-10-310-914A-985	Sequence 985, App
c 35	19.4	31.8	57	16	US-11-036-256-48	Sequence 48, Appl
c 36	19.4	31.8	60	3	US-09-908-975-9618	Sequence 9618, Ap
c 37	19.4	31.8	64	11	US-10-310-914A-17542	Sequence 17542, A
c 38	19.4	31.8	87	16	US-11-036-256-39	Sequence 39, Appl
c 39	19.4	31.8	87	16	US-11-036-256-49	Sequence 49, Appl
c 40	19.4	31.8	87	16	US-11-036-256-50	Sequence 50, Appl
c 41	19.4	31.8	103	16	US-11-043-788-335	Sequence 335, App
c 42	19.4	31.8	116	7	US-10-029-386-23311	Sequence 23311, A
c 43	19.2	31.5	50	7	US-10-131-827-481	Sequence 481, App
c 44	19.2	31.5	66	11	US-10-310-914A-11078	Sequence 11078, A
c 45	19.2	31.5	69	11	US-10-310-914A-6590	Sequence 6590, Ap

ALIGNMENTS

RESULT 1

US-10-310-914A-14543
; Sequence 14543, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14543
; LENGTH: 61
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-14543

Query Match 100.0%; Score 61; DB 11; Length 61;
Matches 48; Conservative 13; Mismatches 0; Indels 0; Gaps 0;
Base Local Similarity 78.7%; Pred. No. 2.8e-11;

Oy 1 AGCTGCCCCCTCTTCTCCCTCACACTACAGCCCTGCTGGGGAGAGGGGGTGGGTC 60
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 60

Oy 61 T 61
Db 61 U 61

RESULT 2

US-11-121-849-23506
; Sequence 23506, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.

; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 23506
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-23506

Query Match 41.0%; Score 25; DB 15; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTCACACTACAGCCCTGTTGGGGGA 45
Db 1 CTCACACTACAGCCCTGTTGGGGGA 25

RESULT 3
US-10-310-914A-14543/c
; Sequence 14543, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14543
; LENGTH: 61
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-14543

Query Match 39.7%; Score 24.2; DB 11; Length 61;
Best Local Similarity 62.3%; Pred. No. 1.5e+02;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AGCTGCCCTCTTCTCCCTCACAACACTACAGCCCTGTTGGGGGAGAGGGGTGGTGC 60
Db 61 AGCACCACCCCTTCTCCCCACCACGGGCTGTAGTGTAGGGGAGAGAGGGGCAGC 2
Qy 61 T 61
Db 1 T 1

RESULT 4
US-10-057-940-7
; Sequence 7, Application US/10057940
; Publication No. US20020168686A1
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; TITLE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12

; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GC-rich tract
US-10-057-940-7

Query Match 38.7%; Score 23.6; DB 6; Length 64;
Best Local Similarity 64.8%; Pred. No. 2.4e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 6 CCCTCCTCTTCTCCCTCACAACACTACAGCCCTGTTGGGGGAGAGGGGTGGGTG 59
Db 2 CCC 55

RESULT 5
US-10-057-940-7/c
; Sequence 7, Application US/10057940
; Publication No. US20020168686A1
; GENERAL INFORMATION:
; APPLICANT: Pantoliano, Michael W.
; APPLICANT: Carver, Jr., Theodore, E.
; TITLE OF INVENTION: High Throughput Method for Functionally Classifying Proteins
; TITLE OF INVENTION: Identified Using a Genomics Approach
; FILE REFERENCE: 1503.0310002/JAG/JSO
; CURRENT APPLICATION NUMBER: US/10/057,940
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/190,128
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/065,129
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GC-rich tract
US-10-057-940-7

Query Match 38.7%; Score 23.6; DB 6; Length 64;
Best Local Similarity 64.8%; Pred. No. 2.4e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 6 CCCTCCTCTTCTCCCTCACAACACTACAGCCCTGTTGGGGGAGAGGGGTGGGTG 59
Db 63 CCC 10

RESULT 6
US-10-310-914A-148966/c
; Sequence 148966, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148966
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-148966

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GTGGGGGAGAGGGGTGGTGC 60
|||
DB 23 GTGGGGGAGAGGGGTGGTGC 1

RESULT 7

US-10-310-914A-148976/c
; Sequence 148976, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148976
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148976

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTCTCTTCTCCCTCACACTA 29
|||
DB 23 CCTCTCTTCTCCCTCACACTA 1

RESULT 8

US-10-310-914A-1065883/c
; Sequence 1065883, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065883
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065883

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GTGGGGGAGAGGGGTGGTGC 60
|||
DB 23 GTGGGGGAGAGGGGTGGTGC 1

RESULT 9

US-10-310-914A-1065889/c
; Sequence 1065889, Application US/10310914A
; Publication No. US20060003322A1

GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065889
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065889

Query Match 37.7%; Score 23; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CCTCTCTTCTCCCTCACACTA 29
|||
DB 23 CCTCTCTTCTCCCTCACACTA 1

RESULT 10

US-10-077-319-92/c
; Sequence 92, Application US/10077319
; Publication No. US20030027781A1

GENERAL INFORMATION:
; APPLICANT: HEILIG, JOSEPH S.
; APPLICANT: GOLD, LARRY
; TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS BY
; EXPONENTIAL ENRICHMENT: TISSUE SELEX
; NUMBER OF SEQUENCES: 240
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/077,319
; FILING DATE: 14-Feb-2002
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/396,002
; FILING DATE: 14-Sep-1999
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; APPLICATION NUMBER: 08/434,001
; FILING DATE: 05-MAY-1995
; APPLICATION NUMBER: 08/906,955
; FILING DATE: 05-AUGUST-1997

ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX30-5/D
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 268-0066
; TELEFAX: (303) 268-0065

INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; SEQUENCE DESCRIPTION: SEQ ID NO: 92:
US-10-077-319-92

Query Match          37.4%; Score 22.8; DB 6; Length 70;
Best Local Similarity 66.0%; Pred. No. 4.5e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy  3 CTGCCCTCTTCTCCCTCACACTACAGCCCTGGTGGGGAGAGGGG 52
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Db  51 CTACCCCTCTCGGCCCAAGTCACTACTGCTAGGAGGCTCACAAACAGG 2

RESULT 11
US-10-310-914A-148933/c
; Sequence 148933, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148933
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148933

Query Match          36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  34 CCTGGTGGGGGAGAGGGGGTG 55
    |||||
Db  22 CCTGGTGGGGGAGAGGGGGTG 1

RESULT 12
US-10-310-914A-148939/c
; Sequence 148939, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148939
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148939

Query Match          36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  36 TGGTGGGGGAGAGGGGGTGGG 57
    |||||
Db  22 TGGTGGGGGAGAGGGGGTGGG 1

RESULT 13
US-10-310-914A-1065861/c
; Sequence 1065861, Application US/10310914A
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065861
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065861

Query Match          36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  34 CCTGGTGGGGGAGAGGGGGTG 55
    |||||
Db  22 CCTGGTGGGGGAGAGGGGGTG 1

RESULT 14
US-10-310-914A-1065867/c
; Sequence 1065867, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065867
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065867

Query Match          36.1%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  36 TGGTGGGGGAGAGGGGGTGGG 57
    |||||
Db  22 TGGTGGGGGAGAGGGGGTGGG 1

RESULT 15
US-10-310-914A-148934/c
; Sequence 148934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148934
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
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US-10-310-914A-148934

Query Match 36.1%; Score 22; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GGGGAGAGGGGGTGGTGCT 61
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Db 23 GGGGAGAGGGGGTGGTGCT 2

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Job time : 848 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:34:34 ; Search time 120 Seconds
(without alignments)
949.806 Million cell updates/sec

Title: US-10-604-926A-1931

Perfect score: 61

Sequence: 1 agctgcctctctctctctcc.....gggagagggtgggtgct 61

Scoring table: IDENTITY NUC

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Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3233144

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Maximum DB seq length: 120

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21.2	34.8	74	7	US-11-234-676-91
3	19.4	31.8	57	9	US-11-036-257-48
C 4	19.4	31.8	87	9	US-11-036-257-39
C 5	19.4	31.8	87	9	US-11-036-257-49
6	19.4	31.8	87	9	US-11-036-257-50
7	19.2	31.5	37	7	US-11-234-676-159
8	18.6	30.5	97	7	US-11-043-842-176
C 9	18.6	30.5	116	7	US-11-356-568A-96
10	18.2	29.8	73	7	US-11-292-078-10537
C 11	18	29.5	120	8	US-11-266-748A-76054
C 12	18	29.5	120	8	US-11-266-748A-109214
C 13	18	29.5	120	8	US-11-266-748A-128865
14	17.6	28.9	101	7	US-11-244-330A-2130
15	17.6	28.9	120	7	US-11-244-330A-2131
16	17.2	28.2	74	7	US-11-234-676-115
C 17	17.2	28.2	77	7	US-11-043-824-115
18	17	27.9	106	7	US-11-429-276-817
19	16.8	27.5	47	7	US-11-370-584-997
20	16.6	27.2	38	6	US-10-551-504-185
21	16.6	27.2	38	6	US-10-551-504-187
C 22	16.6	27.2	47	7	US-11-370-584-2552
23	16.6	27.2	67	7	US-11-292-078-16921

C 24	16.6	27.2	73	6	US-10-523-343-48	Sequence 48, Appl
C 25	16.6	27.2	79	6	US-10-523-343-58	Sequence 58, Appl
C 26	16.6	27.2	88	7	US-11-364-873-117	Sequence 117, Appl
C 27	16.6	27.2	115	8	US-11-266-748A-422367	Sequence 422367,
C 28	16.4	26.9	28	8	US-11-173-889-49	Sequence 49, Appl
C 29	16.4	26.9	45	7	US-11-043-824-176	Sequence 176, Appl
30	16.4	26.9	52	6	US-10-523-647-86	Sequence 86, Appl
31	16.4	26.9	88	6	US-10-834-268-3988	Sequence 3988, Ap
C 32	16.4	26.9	96	8	US-11-301-554-1444	Sequence 1444, Ap
C 33	16.4	26.9	98	9	US-11-376-694-23	Sequence 23, Appl
C 34	16.4	26.9	98	9	US-11-376-694-24	Sequence 24, Appl
C 35	16.4	26.9	103	7	US-11-429-276-1994	Sequence 1994, Ap
36	16.4	26.9	103	7	US-11-429-276-1996	Sequence 1996, Ap
C 37	16.4	26.9	115	9	US-11-314-868-34	Sequence 34, Appl
C 38	16.4	26.9	115	9	US-11-314-868-37	Sequence 37, Appl
C 39	16.2	26.6	32	7	US-11-234-676-160	Sequence 160, Appl
C 40	16.2	26.6	51	8	US-11-143-642-970	Sequence 970, Appl
C 41	16.2	26.6	71	6	US-10-525-817-141	Sequence 141, Appl
C 42	16.2	26.6	78	9	US-11-317-330A-10	Sequence 10, Appl
C 43	16.2	26.6	97	7	US-11-043-842-90	Sequence 90, Appl
C 44	16.2	26.6	104	7	US-11-374-388-18	Sequence 18, Appl
45	16.2	26.6	105	7	US-11-389-343-177	Sequence 177, Appl

ALIGNMENTS

RESULT 1
US-11-234-676-91
; Sequence 91, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; PRIOR FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 74
; TYPE: DNA
; FEATURE:
; OTHER INFORMATION: synthetic aptamer
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(74)
; OTHER INFORMATION: all purines (A and G) are deoxy, all pyrimidines (C and U) are
; OTHER INFORMATION: 2'-O-methyl
US-11-234-676-91

Query Match 34.8%; Score 21.2; DB 7; Length 74;
Best Local Similarity 64.7%; Pred. NO. 5.4e+02;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCTGGTGGGAGAGGGGTGGTGC 60

DB 19 CUACAGCCCGGUGGGCGGCAUUGGUGGAUC 52

```
RESULT 2
US-11-234-676-94
; Sequence 94, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; FILE OF INVENTION: Autoimmune Disease Therapeutics
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; PRIOR FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 74
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: synthetic aptamer
; NAME/KEY: modified base
; LOCATION: (1)..(74)
; OTHER INFORMATION: all purines (A and G) are deoxy, all pyrimidines (C and U) are
; OTHER INFORMATION: 2'-O-methyl
US-11-234-676-94

Query Match 34.8%; Score 21.2; DB 7; Length 74;
Best Local Similarity 64.7%; Pred. No. 5.4e+02;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCCTGTGGGGAGAGAGGGGGTGGTGC 60
|:|||||:|||||:|||||:|||||:|||||:
Db 19 CUACAGCGCGGUGGUGGCGCAUAGGUGGGAUGC 52
|:|||||:|||||:|||||:|||||:|||||:

RESULT 3
US-11-036-257-48
; Sequence 48, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 48

Query Match 34.8%; Score 21.2; DB 7; Length 74;
Best Local Similarity 64.7%; Pred. No. 5.4e+02;
Matches 22; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 27 CTACAGCCCTGTGGGGAGAGAGGGGGTGGTGC 60
|:|||||:|||||:|||||:|||||:|||||:
Db 19 CUACAGCGCGGUGGUGGCGCAUAGGUGGGAUGC 52
|:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-11-036-257-39/c
; Sequence 39, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 39
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-036-257-39

Query Match 31.8%; Score 19.4; DB 9; Length 87;
Best Local Similarity 79.3%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 TACAGCCCTGTGGGGGAGAGAGGGGGTGG 56
|:|||||:|||||:|||||:|||||:|||||:
Db 8 TACAGCTATGGCTGGGGAGAGAGGGGGATGG 36
|:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-11-036-257-49/c
; Sequence 49, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 49
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; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-036-257-48
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Query Match 31.8%; Score 19.4; DB 9; Length 57;
Best Local Similarity 79.3%; Pred. No. 2e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 TACAGCCCTGTGGGGGAGAGAGGGGGTGG 56
|:|||||:|||||:|||||:|||||:|||||:
Db 8 TACAGCTATGGCTGGGGAGAGAGGGGGATGG 36
|:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 4
US-11-036-257-39/c
; Sequence 39, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 39
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-036-257-39
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```
Query Match 31.8%; Score 19.4; DB 9; Length 87;
Best Local Similarity 79.3%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 28 TACAGCCCTGTGGGGGAGAGAGGGGGTGG 56
|:|||||:|||||:|||||:|||||:|||||:
Db 80 TACAGCTATGGCTGGGGAGAGAGGGGGATGG 52
|:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 5
US-11-036-257-49/c
; Sequence 49, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE OF INVENTION: THEIR USE
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 49
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; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 49
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (13)..(72)
US-11-036-257-49

Query Match 31.8%; Score 19.4; DB 9; Length 87;
Best Local Similarity 79.3%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 28 TACAGCCCTGTGGGGAGAGGGGGTGG 56
||||| ||| ||||| ||||| ||||| |||||
Db 80 TACAGCTATGGCTGGGAGAGGGGATGG 52

RESULT 6

; Sequence 50, Application US/11036257
; Publication No. US20060148680A1
; GENERAL INFORMATION:
; APPLICANT: KIELISZEWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; APPLICANT: KOPCHICK, JOHN J.
; APPLICANT: OKADA, SHIGERU
; TITLE OF INVENTION: GLYCOPROTEINS PRODUCED IN PLANTS AND METHODS OF
; FILE REFERENCE: 27211/04081
; CURRENT APPLICATION NUMBER: US/11/036,257
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-036-257-50

Query Match 31.8%; Score 19.4; DB 9; Length 87;
Best Local Similarity 79.3%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 28 TACAGCCCTGTGGGGAGAGGGGGTGG 56
||||| ||| ||||| ||||| ||||| |||||
Db 8 TACAGCTATGGCTGGGAGAGGGGATGG 36

RESULT 7

; Sequence 159, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.

; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 159
; LENGTH: 37
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: synthetic aptamer
; NAME/KEY: modified base
; LOCATION: (1)..(37)
; OTHER INFORMATION: all purines (A and G) are deoxy, all pyrimidines (C and U) are
; OTHER INFORMATION: 2'-O-methyl
US-11-234-676-159

Query Match 31.5%; Score 19.2; DB 7; Length 37;
Best Local Similarity 65.6%; Pred. No. 2.1e+03;
Matches 21; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 29 ACAGCCCTGTGGGGAGAGGGGGTGGTGC 60
||||| ||| ||||| ||||| ||||| |||||
Db 1 ACAGCGCGGUGGGCGGCAUUGGGUGGAGC 32

RESULT 8

; Sequence 176, Application US/11043842
; Publication No. US20060183131A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1004
; CURRENT APPLICATION NUMBER: US/11/043,842
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1028
; SEQ ID NO 176
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-043-842-176

Query Match 30.5%; Score 18.6; DB 7; Length 97;
Best Local Similarity 61.2%; Pred. No. 4.3e+03;
Matches 30; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 7 CCTCCTCTTCTCCCTCACACTACAGCCCTGTGGGGAGAGGGGGTGG 55
||||| ||| ||||| ||||| ||||| |||||
Db 24 CCTCACCTCTCCCGCGCTCTGGCGCCCGGCTCTGGCGAAGCTGCTG 72

RESULT 9

US-11-356-568A-96/c

```

; Sequence 96, Application US/11356568A
; Publication No. US20060188981A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Adrian
; TITLE OF INVENTION: Ratcliffe, Peter
; FILE REFERENCE: D-0021.5C-3
; CURRENT APPLICATION NUMBER: US/11/356,568A
; CURRENT FILING DATE: 2006-02-17
; PRIOR APPLICATION NUMBER: 10/319,003
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/341,036
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 96
; LENGTH: 116
; TYPE: DNA
; ORGANISM: HUMAN
US-11-356-568A-96

Query Match      30.5%; Score 18.6; DB 7; Length 116;
Best Local Similarity 57.9%; Pred. No. 4.6e+03;
Matches 33; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 5 GCCCTCTCTCTCCCTCACACTACAGCCCTGTTGGGGGAGAGGGGGTGGTCT 61
Db 57 GCCCTGTCCTCTCTCCCCCATACCAAGCTAGGATGGGGGTGGAGTGGGGCGCAGGT 1

RESULT 10
US-11-292-078-10537
; Sequence 10537, Application US/11292078
; Publication No. US20060195941A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 16517.346 - 38-21(52274)C
; CURRENT APPLICATION NUMBER: US/11/292,078
; CURRENT FILING DATE: 2005-12-02
; PRIOR APPLICATION NUMBER: US 10/021,323
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255,619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 10537
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3828-028-Q6-N6-B4
US-11-292-078-10537

Query Match      29.8%; Score 18.2; DB 7; Length 73;
Best Local Similarity 61.7%; Pred. No. 5.5e+03;
Matches 29; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 8 CTCCTCTCTCTCCCTCACACTACAGCCCTGTTGGGGGAGAGGGGGT 54
Db 8 CCCCCCTTTTCCCCCCCCCCCCCCCCCTTTTGGGGGGGGGTGTGT 54

RESULT 11
US-11-266-748A-76054/C
; Sequence 76054, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick

```

```

; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 76054
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-76054

Query Match      29.5%; Score 18; DB 8; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 32 GCCCTGCTGGGGGAGAGGGGGTGGG 57
Db 26 GCTAGGGTAGGGGAGATGGGGGTGGG 1

RESULT 12
US-11-266-748A-109214/C
; Sequence 109214, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 109214
; LENGTH: 120
; TYPE: DNA

```

```

; ORGANISM: Homo Sapiens
US-11-266-748A-109214

Query Match      29.5%; Score 18; DB 8; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 32 GCCTGCTGGGAGAGGGGTGGG 57
DB 26 GCTAGGGTAGGGAGATGGGGTGGG 1

RESULT 13
US-11-266-748A-128865
; Sequence 128865, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 128865
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-128865

Query Match      29.5%; Score 18; DB 8; Length 120;
Best Local Similarity 80.8%; Pred. No. 7.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 32 GCCTGCTGGGAGAGGGGTGGG 57
DB 95 GCTAGGGTAGGGAGATGGGGTGGG 120

RESULT 14
US-11-244-330A-2130
; Sequence 2130, Application US/11244330A
; Publication No. US20060195932A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, Nordine
; APPLICANT: Liu, Jingdong
; APPLICANT: Miller, Phillip W.
; APPLICANT: O Connell, Keith M.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: With the Carbon Assimilation Pathway
; FILE REFERENCE: 16517.339 (38-21(15091)D/US)
; CURRENT APPLICATION NUMBER: US/11/244,330A
; CURRENT FILING DATE: 2005-10-06
; PRIOR APPLICATION NUMBER: US 09/987,899
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/262,979
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: US 60/076,712
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 7341
; SEQ ID NO 2131
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Zea mays
US-11-244-330A-2131

Query Match      28.9%; Score 17.6; DB 7; Length 120;
Best Local Similarity 65.0%; Pred. No. 1e+04;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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DB 41 TGCTCTCCGCTACACCGTGCCACTCCAGCAGGGGGCGG 80

Search completed: October 14, 2006, 19:38:23
Job time : 121 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:36:24 ; Search time 2007 Seconds
(without alignments)
605.382 Million cell updates/sec

Title: US-10-604-926A-4539

Perfect score: 19

Sequence: 1 ggagaagggtgggtgct 19

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 1796954

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

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5: gb_pr.*

6: gb_ro.*

7: gb_sta.*

8: gb_sy.*

9: gb_un.*

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13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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433	11	57..9	21	2	AX167173 Sequence	C 506	11	57..9	30	5	AX785962 Sequence
434	11	57..9	21	2	AX235480 Sequence	C 507	10..8	56..8	14	2	BD137817 Protein e
435	11	57..9	22	2	AX5399 Sequence 69	C 508	10..8	56..8	14	2	AR575807 Sequence
436	11	57..9	22	2	AR061204 Sequence	C 509	10..8	56..8	15	2	AS0780 Sequence 1
437	11	57..9	22	2	CQ760253 Sequence	C 510	10..8	56..8	15	2	AS0781 Sequence 2
438	11	57..9	22	2	DD176305 Verificat	C 511	10..8	56..8	15	2	AR109974 Sequence
439	11	57..9	22	2	AX804044 Sequence	C 512	10..8	56..8	15	2	AR109975 Sequence
440	11	57..9	22	5	S90290S1 {deletion 4	C 513	10..8	56..8	15	2	I33987 Sequence 1
441	11	57..9	24	2	A04020 Sequence 47	C 514	10..8	56..8	15	2	I33988 Sequence 2
442	11	57..9	24	2	AR175900 Sequence	C 515	10..8	56..8	16	2	AX284046 Sequence
443	11	57..9	24	2	CQ816817 Sequence	C 516	10..8	56..8	17	2	AR045385 Sequence
444	11	57..9	24	2	AX815865 Sequence	C 517	10..8	56..8	17	2	BD259257 Regulation
445	11	57..9	25	2	A71353 Sequence 4	C 518	10..8	56..8	17	2	BD266424 Universal
446	11	57..9	25	2	AR142053 Sequence	C 519	10..8	56..8	17	2	CQ617572 Sequence
447	11	57..9	25	2	BD022424 Multi-fun	C 520	10..8	56..8	17	2	CQ617573 Sequence
448	11	57..9	25	2	BD235883 Detection	C 521	10..8	56..8	17	2	CQ617574 Sequence
449	11	57..9	25	2	CS017966 Sequence	C 522	10..8	56..8	17	2	CQ617575 Sequence
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451	11	57..9	25	2	CS186713 Sequence	C 524	10..8	56..8	17	2	CQ622053 Sequence
452	11	57..9	25	2	AR202255 Sequence	C 525	10..8	56..8	17	2	DD186215 Probe set
453	11	57..9	25	2	AR223257 Sequence	C 526	10..8	56..8	17	2	DD188174 Probe set
454	11	57..9	25	2	I59920 Sequence 47	C 527	10..8	56..8	17	2	I37578 Sequence 59
455	11	57..9	25	2	I86778 Sequence 47	C 528	10..8	56..8	17	2	AR286483 Sequence
456	11	57..9	25	2	I95803 Sequence 47	C 529	10..8	56..8	17	2	I52437 Sequence 17

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C 533	10.8	56.8	17	2	AR458636	AR458636 Sequence	606	10.8	56.8	24	2	AR052981	AR052981 Sequence
C 534	10.8	56.8	17	2	AR458637	AR458637 Sequence	607	10.8	56.8	24	2	BD229114	BD229114 Endogeneo
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C 545	10.8	56.8	18	2	AX923497	AX923497 Sequence	C 618	10.8	56.8	25	2	AR055503	AR055503 Sequence
C 546	10.8	56.8	18	2	BD190823	BD190823 G-rich ol	C 619	10.8	56.8	25	2	AR055512	AR055512 Sequence
C 547	10.8	56.8	18	2	BD190838	BD190838 G-rich ol	C 620	10.8	56.8	25	2	AR085386	AR085386 Sequence
C 548	10.8	56.8	18	2	CQ784357	CQ784357 Sequence	C 621	10.8	56.8	25	2	AR085395	AR085395 Sequence
C 549	10.8	56.8	18	2	DD162379	DD162379 Transgeni	C 622	10.8	56.8	25	2	CQ620501	CQ620501 Sequence
C 550	10.8	56.8	18	2	AR570260	AR570260 Sequence	C 623	10.8	56.8	25	2	CQ620502	CQ620502 Sequence
C 551	10.8	56.8	18	2	AX767745	AX767745 Sequence	C 624	10.8	56.8	25	2	CQ620503	CQ620503 Sequence
C 552	10.8	56.8	18	2	AX796219	AX796219 Sequence	C 625	10.8	56.8	25	2	CQ620504	CQ620504 Sequence
C 553	10.8	56.8	18	2	AX796220	AX796220 Sequence	C 626	10.8	56.8	25	2	CQ620505	CQ620505 Sequence
C 554	10.8	56.8	19	2	BD226531	BD226531 Method an	C 627	10.8	56.8	25	2	CQ620506	CQ620506 Sequence
C 555	10.8	56.8	19	2	DD192671	DD192671 Method fo	C 628	10.8	56.8	25	2	CQ620507	CQ620507 Sequence
C 556	10.8	56.8	19	2	AR295127	AR295127 Sequence	C 629	10.8	56.8	25	2	CQ620508	CQ620508 Sequence
C 557	10.8	56.8	19	2	AX404233	AX404233 Sequence	C 630	10.8	56.8	25	2	CQ620509	CQ620509 Sequence
C 558	10.8	56.8	19	2	AX477615	AX477615 Sequence	C 631	10.8	56.8	25	2	CQ620510	CQ620510 Sequence
C 559	10.8	56.8	19	2	AX482168	AX482168 Sequence	C 632	10.8	56.8	25	2	CQ620511	CQ620511 Sequence
C 560	10.8	56.8	19	2	AX505035	AX505035 Sequence	C 633	10.8	56.8	25	2	CQ620512	CQ620512 Sequence
C 561	10.8	56.8	19	2	AX511407	AX511407 Sequence	C 634	10.8	56.8	25	2	CQ626941	CQ626941 Sequence
C 562	10.8	56.8	19	2	AX659401	AX659401 Sequence	C 635	10.8	56.8	25	2	CQ626953	CQ626953 Sequence
C 563	10.8	56.8	19	2	AX721768	AX721768 Sequence	C 636	10.8	56.8	25	2	CQ862047	CQ862047 Sequence
C 564	10.8	56.8	20	2	A26760	A26760 Oligonucleo	C 637	10.8	56.8	25	2	CQ862090	CQ862090 Sequence
C 565	10.8	56.8	20	2	AR004444	AR004444 Sequence	C 638	10.8	56.8	25	2	CQ866554	CQ866554 Sequence
C 566	10.8	56.8	20	2	AR126694	AR126694 Sequence	C 639	10.8	56.8	25	2	CQ866555	CQ866555 Sequence
C 567	10.8	56.8	20	2	BD143391	BD143391 Human bla	C 640	10.8	56.8	25	2	CQ890003	CQ890003 Sequence
C 568	10.8	56.8	20	2	BD226640	BD226640 Methods f	C 641	10.8	56.8	25	2	CS010247	CS010247 Sequence
C 569	10.8	56.8	20	2	CQ754283	CQ754283 Sequence	C 642	10.8	56.8	25	2	CS122162	CS122162 Sequence
C 570	10.8	56.8	20	2	CQ876459	CQ876459 Sequence	C 643	10.8	56.8	25	2	AR342808	AR342808 Sequence
C 571	10.8	56.8	20	2	CQ975224	CQ975224 Sequence	C 644	10.8	56.8	25	2	AR441869	AR441869 Sequence
C 572	10.8	56.8	20	2	CS011689	CS011689 Sequence	C 645	10.8	56.8	25	2	AR461564	AR461564 Sequence
C 573	10.8	56.8	20	2	DD174360	DD174360 SELECTION	C 646	10.8	56.8	25	2	AR461565	AR461565 Sequence
C 574	10.8	56.8	20	2	DD177122	DD177122 Verificat	C 647	10.8	56.8	25	2	AR461566	AR461566 Sequence
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C 577	10.8	56.8	20	2	AR314287	AR314287 Sequence	C 650	10.8	56.8	25	2	AR461569	AR461569 Sequence
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C 579	10.8	56.8	20	2	AR317237	AR317237 Sequence	C 652	10.8	56.8	25	2	AR461571	AR461571 Sequence
C 580	10.8	56.8	20	2	AR453337	AR453337 Sequence	C 653	10.8	56.8	25	2	AR461572	AR461572 Sequence
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C 582	10.8	56.8	20	2	AR652614	AR652614 Sequence	C 655	10.8	56.8	25	2	AR461574	AR461574 Sequence
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C 584	10.8	56.8	20	2	AX665475	AX665475 Sequence	C 657	10.8	56.8	25	2	AR468004	AR468004 Sequence
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C 586	10.8	56.8	21	2	A71398	A71398 Sequence 9	C 659	10.8	56.8	25	2	AR527646	AR527646 Sequence
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C 589	10.8	56.8	21	2	BD269904	BD269904 Tumor nec	C 662	10.8	56.8	25	2	AX453028	AX453028 Sequence
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C 591	10.8	56.8	21	2	CS122028	CS122028 Sequence	C 664	10.8	56.8	26	2	CS097996	CS097996 Sequence
C 592	10.8	56.8	21	2	CS122107	CS122107 Sequence	C 665	10.8	56.8	27	2	AX538003	AX538003 Sequence
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C 594	10.8	56.8	21	2	CS227039	CS227039 Sequence	C 667	10.8	56.8	28	2	A57793	A57793 Sequence 6
C 595	10.8	56.8	21	2	CS227040	CS227040 Sequence	C 668	10.8	56.8	28	2	AR120087	AR120087 Sequence
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C 597	10.8	56.8	21	2	AR287735	AR287735 Sequence	C 670	10.8	56.8	28	2	AR120089	AR120089 Sequence
C 598	10.8	56.8	21	2	AR381137	AR381137 Sequence	C 671	10.8	56.8	28	2	BD141804	BD141804 Novel G p
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C 600	10.8	56.8	21	2	AX023396	AX023396 Sequence	C 673	10.8	56.8	28	2	BD181755	BD181755 Novel G p
C 601	10.8	56.8	23	2	CS014378	CS014378 Sequence	C 674	10.8	56.8	28	2	CS144091	CS144091 Sequence
C 602	10.8	56.8	23	2	CS150594	CS150594 Sequence	C 675	10.8	56.8	28	2	CS144092	CS144092 Sequence

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C 678	10.8	56.8	28	2	I41113	I41113 Sequence 16	C 751	10.6	55.8	20	2	CS130456	CS130456 Sequence
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C 681	10.8	56.8	29	2	BD081646	BD081646 Secreted	C 754	10.6	55.8	20	2	DD174870	DD174870 THERAPEUT
C 682	10.8	56.8	29	2	CS077900	CS077900 Sequence	C 755	10.6	55.8	20	2	DD174885	DD174885 THERAPEUT
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C 685	10.8	56.8	29	2	CS097995	CS097995 Sequence	C 758	10.6	55.8	20	2	DD175032	DD175032 THERAPEUT
C 686	10.8	56.8	29	2	CS111435	CS111435 Sequence	C 759	10.6	55.8	20	2	DD175167	DD175167 THERAPEUT
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C 688	10.8	56.8	29	2	CS111437	CS111437 Sequence	C 761	10.6	55.8	20	2	I20432	I20432 Sequence 11
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C 701	10.8	56.8	30	2	CS116813	CS116813 Sequence	C 774	10.6	55.8	20	2	AR477475	AR477475 Sequence
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C 718	10.6	55.8	18	2	AX599828	AX599828 Sequence	C 791	10.6	55.8	21	2	AR168255	AR168255 Sequence
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C 723	10.6	55.8	19	2	CS015376	CS015376 Sequence	C 796	10.6	55.8	21	2	AX045693	AX045693 Sequence
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C 727	10.6	55.8	19	2	AX810948	AX810948 Sequence	C 800	10.6	55.8	21	2	AX304980	AX304980 Sequence
C 728	10.6	55.8	20	2	A70728	A70728 Sequence 49	C 801	10.6	55.8	21	2	AX306509	AX306509 Sequence
C 729	10.6	55.8	20	2	A79212	A79212 Sequence 44	C 802	10.6	55.8	21	2	AX553598	AX553598 Sequence
C 730	10.6	55.8	20	2	AR023991	AR023991 Sequence	C 803	10.6	55.8	21	8	AB214035	AB214035 Synthetic
C 731	10.6	55.8	20	2	AR050657	AR050657 Sequence	C 804	10.6	55.8	22	2	BD011200	BD011200 Human tel
C 732	10.6	55.8	20	2	AR074213	AR074213 Sequence	C 805	10.6	55.8	22	2	BD261048	BD261048 Assay for
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ALIGNMENTS

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BD182432 30 bp DNA linear PAT 15-MAY-2003
LOCUS Human artificial chromosomes comprising human antibody light chain
DEFINITION lambda gene, and non-human animals retaining human artificial
chromosome transmittable to progeny.
ACCESSION BD182432.1 GI:30793350
VERSION WO 02092812-A/7.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1. (bases 1 to 30)
AUTHORS Kuroiwa,Y.,Tomizuka,K., Yoshida,H. and Ishida,I.
TITLE Human artificial chromosomes comprising human antibody light chain
lambda gene, and non-human animals retaining human artificial
chromosome transmittable to progeny
JOURNAL Patent: WO 02092812-A 7 21-NOV-2002;
COMMENT KIRIN BREWERY CO LTD,YOSHIMI KUROIWA,KAZUMA TOMIZUKA, HITOSHI
YOSHIDA, ISAO ISHIDA
OS Artificial Sequence
PN WO 02092812-A/7
PD 21-NOV-2002
PF 10-MAY-2002 WO 2002JP004587
PR 11-MAY-2001 JP 01P 142371
PI YOSHIMI KUROIWA,KAZUMA TOMIZUKA,HITOSHI YOSHIDA,ISAO ISHIDA PC
C12N15/09,A01K67/027,C07K16/00,C12P21/08
CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
FT source 1. .30
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DB 19 GGAGAGGGGTGGG 5
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CS092194 19 bp RNA linear PAT 03-JUN-2005
LOCUS Sequence 268 from Patent WO2005045032.
DEFINITION CS092194
ACCESSION CS092194
VERSION CS092194.1 GI:66949741
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Usman,N. and McSWIGGEN,J.
TITLE RNA interference mediated inhibition of early growth response gene
expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045032-A 268 19-MAY-2005;
Sirma Therapeutics, Inc. (US)
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DB 2 GAAGAAAGAGTGGGTGCT 20
RESULT 2
CS092020 19 bp RNA linear PAT 03-JUN-2005
LOCUS Sequence 94 from Patent WO2005045032.
DEFINITION CS092020
ACCESSION CS092020
VERSION CS092020.1 GI:66949567
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Usman,N. and McSWIGGEN,J.
TITLE RNA interference mediated inhibition of early growth response gene
expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045032-A 94 19-MAY-2005;
Sirma Therapeutics, Inc. (US)
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DEFINITION Sequence 23 from patent US 6929912.
ACCESSION AR704960
VERSION AR704960.1 GI:75923278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Guida, M., Hall, J., Petros, W.P., Vredenburg, J.J., Colvin, O.M. and Marks, J.R.
TITLE Methods for evaluating the ability to metabolize pharmaceuticals
JOURNAL Patent: US 6929912-A 23 16-AUG-2005;
Genaisance Pharmaceuticals, Inc. and Duke University; New Haven, CT

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source Location/Qualifiers
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ORIGIN
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DEFINITION Sequence 9827 from patent US 6537751.
ACCESSION AR298092
VERSION AR298092.1 GI:31685376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9827 25-MAR-2003;
Genet S.A.;;
FRX;

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RESULT 6
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DEFINITION Sequence 21 from patent US 6962776.
ACCESSION AR761712
VERSION AR761712.1 GI:83330324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kopecky, S.L., Goronszy, J.J. and Weyand, C.M.
TITLE Methods and materials for evaluating cardiovascular conditions
JOURNAL Patent: US 6962776-A 21 08-NOV-2005;
Mayo Foundation for Medical Education and Research; Rochester, MN

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LOCUS AR125125 25 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 12 from patent US 6177086.
ACCESSION AR125125
VERSION AR125125.1 GI:14111187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Riley, L.W., Nathan, C.F. and Ehrh, S.
TITLE DNA molecule conferring on Mycobacterium tuberculosis resistance
against antimicrobial reactive oxygen and nitrogen intermediates
JOURNAL Patent: US 6177086-A 12 23-JAN-2001;
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Db 1 GGGGATGGGTGGGTGC 18

RESULT 8
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LOCUS AR030170 27 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 359 from patent US 5861244.
ACCESSION AR030170
VERSION AR030170.1 GI:5943384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 359 19-JAN-1999;
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CS025768/c
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DEFINITION Sequence 20 from Patent WO2005014029.
ACCESSION CS025768
VERSION CS025768.1 GI:60496425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Onichtchouk,D.
TITLE Use of dg008, dg065, dg210 or dg 239 secreted protein products for preventing and treating pancreatic diseases and/or obesity and/or metabolic syndrome
JOURNAL Patent: WO 2005014029-A 20 17-FEB-2005;
DEVELOP DeveloGen Aktiengesellschaft fuer entwicklungsbiologische Forschung (DE)
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Db 20 AGTAGGGTGTGGGTGC 5

RESULT 10
CS015778/c
LOCUS CS015778 30 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 5 from Patent WO2005007198.
ACCESSION CS015778
VERSION CS015778.1 GI:59675351
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Chang,X.J.
TITLE Disease specific agents for diagnostics and therapeutics
JOURNAL Patent: WO 2005007198-A 5 27-JAN-2005;
ATTORNEY AttoGen, Inc. (US)
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Db 23 AGAGGGGAGTGGGTGC 8

RESULT 11
AX207085/c
LOCUS AX207085 25 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 38 from Patent WO0153476.
ACCESSION AX207085
VERSION AX207085.1 GI:15394882
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
AUTHORS Bruce,W.B. and Niu,X.
TITLE Novel plant promoters and methods of use
JOURNAL Patent: WO 0153476-A 38 26-JUL-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1. .25
/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"

ORIGIN

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 2; Length 25;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
Db 25 GGAGAAGGAGTGAAGCT 7

RESULT 12
AX785961/c
LOCUS AX785961 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 470 from Patent WO03050299.
ACCESSION AX785961
VERSION AX785961.1 GI:32953581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cullen,P. and Seedorf,U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 470 19-JUN-2003;
OGHAM GmbH (DE)
FEATURES
source Location/Qualifiers
1. .30
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 2; Length 30;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
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Db 23 GCAGGAGGAGGGGGCT 5

RESULT 13
LOCUS AR173370/c
DEFINITION Sequence 4 from patent US 6303847.
ACCESSION AR173370
VERSION AR173370.1 GI:17912861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kawaoka,A. and Ebinuma,H.
TITLE DNA encoding a transcription factor controlling phenylpropanoid biosynthesis pathway
JOURNAL Patent: US 6303847-A 4 16-OCT-2001;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGTG 17
|||||
Db 17 GAAGGGGGTGGTG 4

RESULT 14
LOCUS AR096649
DEFINITION Sequence 33 from patent US 6008048.
ACCESSION AR096649
VERSION AR096649.1 GI:10025634
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowser,L.M.
TITLE Antisense inhibition of EGR-1 expression
JOURNAL Patent: US 6008048-A 33 28-DEC-1999;
FEATURES
source Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 18;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGG 14
|||||
Db 5 GGAGAGGGGGTGG 18

RESULT 15
LOCUS CS095398/c
DEFINITION Sequence 90 from Patent WO2005045035.
ACCESSION CS095398
VERSION CS095398.1 GI:66951985
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Mcswiggen,J., Chowrira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 90 19-MAY-2005;
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Target Sequence/siNA sense region"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGG 14
|||||
Db 17 GGAGATGGGGTGG 4

RESULT 16
LOCUS CS095497
DEFINITION Sequence 189 from Patent WO2005045035.
ACCESSION CS095497
VERSION CS095497.1 GI:66952084
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Mcswiggen,J., Chowrira,B.M. and Haerberli,P.
TITLE RNA interference mediated inhibition of NOGO and NOGO receptor gene expression using short interfering Nucleic Acid (siNA)
JOURNAL Patent: WO 2005045035-A 189 19-MAY-2005;
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: siNA antisense region"

ORIGIN

Query Match 65.3%; Score 12.4; DB 2; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGG 14
|||||
Db 3 GGAGATGGGGTGG 16

RESULT 17
LOCUS AX826824/c
DEFINITION Sequence 46 from Patent WO03072823.
ACCESSION AX826824
VERSION AX826824.1 GI:39752338
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.

AUTHORS Grandchamp,B. and Mentre,F.
TITLE Method for in vitro detection of cancers by highlighting allelic imbalances in insertion/deletion markers
JOURNAL Patent: WO 03072823-A 46 04-SEP-2003;
ASSISTANCE PUBLIQUE, HOPITAUX DE PARIS (FR)

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FEATURES
source
  Location/Qualifiers
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  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="SEQUENCE DESCRIPTION artificielle: amorce"
ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.9e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGG 14
Db 16 GGAGAAGGGGGTGG 3
RESULT 18
LOCUS AR529043 21 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 246 from patent US 6727063.
ACCESSION AR529043
VERSION AR529043.1 GI:53917480
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: US 6727063-A 246 27-APR-2004; Millennium Pharmaceuticals, Inc. and Whitehead Institute for Biomedical Research; Cambridge, MA
FEATURES
source
  Location/Qualifiers
  1..21
  /organism="unknown"
  /mol_type="genomic DNA"
ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 1.9e+05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAAGGGGGTGGTGCT 19
Db 3 GAAGAGGGGGGTACT 18
RESULT 19
LOCUS AX095068 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 246 from Patent WO0118250.
ACCESSION AX095068
VERSION AX095068.1 GI:13511271
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.O. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 246 15-MAR-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
  Location/Qualifiers
  1..21
  /organism="Homo sapiens"
  /mol_type="unassigned DNA"
  /db_xref="taxon:9606"
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ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 21;
Best Local Similarity 81.2%; Pred. No. 1.9e+05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 4 GAAGGGGGTGGTGCT 19
Db 3 GAAGAGGGGGGTACT 18
RESULT 20
LOCUS AR129481/c 22 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 64 from patent US 6187533.
ACCESSION AR129481
VERSION AR129481.1 GI:14117378
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Bell,G.I., Yamagata,K., Oda,N., Kaisaki,P.J., Furuta,H., Horikawa,Y. and Menzel,S.
TITLE Mutations in the diabetes susceptibility genes hepatocyte nuclear factor (HNF) 1 alpha (.alpha.), HNF1.beta. and HNF4.alpha
JOURNAL Patent: US 6187533-A 64 13-FEB-2001;
FEATURES
source
  Location/Qualifiers
  1..22
  /organism="unknown"
  /mol_type="unassigned DNA"
ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGG 14
Db 14 GGAGTAGGGGGTGG 1
RESULT 21
LOCUS E29389/c 22 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for determining contents of nucleic acids in nucleic acid mixture sample.
ACCESSION E29389
VERSION E29389.1 GI:13020995
KEYWORDS JP 1999281618-A/3.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS Toshihiro,T., Masatoshi,K. and Ryuji,K.
TITLE Method for determining contents of nucleic acids in nucleic acid mixture sample
JOURNAL Patent: JP 1999281618-A 3 15-OCT-1999; SHIZUOKA INST OF SCI & TECHNOL,SRL INC
COMMENT OS Unidentified
PN JP 1999281618-A/3
PD 15-OCT-1999
PF 30-MAR-1998 JP 1998101989
PR
PI TOSHIHIRO TSUNEYOSHI,MASATOSHI KAJI,RYUJI KAWAGUCHI PC
CC G01N27/447,C12Q1/68
FT Key Location/Qualifiers
FT source 1..22 /organism='Unidentified'.
FT Location/Qualifiers
FT source 1..22 /organism='unidentified'
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ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGT 16
    ||||| ||||| |||||
Db 22 AGAAGTGGGTGGGT 9

RESULT 22
E30525/c
LOCUS      22 bp DNA linear PAT 18-JUN-2001
DEFINITION Nucleic acid primer for distinguishing eel species and method for
            distinguishing eel species by using the same.
E30525
ACCESSION  E30525.1 GI:13021474
VERSION     JP 1999276179-A/3.
KEYWORDS   unidentifed
SOURCE      unidentifed
ORGANISM    unclassified sequences.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Toshihiro,T. and Masatoshi,K.
TITLE       Nucleic acid primer for distinguishing eel species and method for
            distinguishing eel species by using the same
JOURNAL     Patent: JP 1999276179-A 3 12-OCT-1999;
COMMENT     SHIZUOKA INST OF SCI & TECHNOL,SRL INC
OS          Unidentifed
PN          JP 1999276179-A/3
PD          12-OCT-1999
PF          30-MAR-1998 JP 1998102209
PR
PT
PI          TOSHIHIRO TSUNEYOSHI,MASATOSHI KAJI
PC          C12N15/09,A01K61/00,C12Q1/68,C12N15/00
CC
FH          Key
FT          source
FT          Location/Qualifiers
            /organism='Unidentifed'.
FEATURES
source
ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 22;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGT 16
    ||||| ||||| |||||
Db 22 AGAAGTGGGTGGGT 9

RESULT 23
CS210348/c
LOCUS      24 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 170 from Patent WO2005111232.
ACCESSION  CS210348
VERSION     CS210348.1 GI:83687387
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Hermeking,H.
TITLE       Silencing of tumor-suppressive genes by cpG-methylation in prostate
            cancer
JOURNAL     Patent: WO 2005111232-A 170 24-NOV-2005;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V.

ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 24;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTG 17
    ||||| ||||| |||||
Db 22 GAAGGGGGTGGGTG 9

RESULT 24
CS210350/c
LOCUS      24 bp DNA linear PAT 15-DEC-2005
DEFINITION Sequence 172 from Patent WO2005111232.
ACCESSION  CS210350
VERSION     CS210350.1 GI:83687389
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Hermeking,H.
TITLE       Silencing of tumor-suppressive genes by cpG-methylation in prostate
            cancer
JOURNAL     Patent: WO 2005111232-A 172 24-NOV-2005;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V.
            Berlin (DE)
FEATURES
source
ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 24;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTG 17
    ||||| ||||| |||||
Db 22 GAAGGGGGTGGGTG 9

RESULT 25
AX548302/c
LOCUS      25 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 226 from Patent WO0240716.
ACCESSION  AX548302
VERSION     AX548302.1 GI:25813336
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Palm,K.
TITLE       Profiling tumor specific markers for the diagnosis and treatment of
            neoplastic disease
JOURNAL     Patent: WO 0240716-A 226 23-MAY-2002;
            Cemines, LLC (US)
FEATURES
source
ORIGIN
Query Match          65.3%; Score 12.4; DB 2; Length 24;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTG 17
    ||||| ||||| |||||
Db 22 GAAGGGGGTGGGTG 9

RESULT 26
AX548302/c
LOCUS      25 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 226 from Patent WO0240716.
ACCESSION  AX548302
VERSION     AX548302.1 GI:25813336
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Palm,K.
TITLE       Profiling tumor specific markers for the diagnosis and treatment of
            neoplastic disease
JOURNAL     Patent: WO 0240716-A 226 23-MAY-2002;
            Cemines, LLC (US)
FEATURES
source
ORIGIN
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Query Match      65.3%; Score 12.4; DB 2; Length 25;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 GAGAAGGGGGTGGG 15
    ||||| |||||
Db  14 GAGAAGGGCGTGGG 1

RESULT 26
LOCUS AR658517/c
DEFINITION Sequence 191 from patent US 6897053.
ACCESSION AR658517
VERSION AR658517.1 GI:67593124
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS O'Donnell,M.E. and Yurieva,O.
TITLE Enzymes derived from thermophilic organisms that function as a
        chromosomal replicase, preparation and use thereof
JOURNAL Patent: US 6897053-A 191 24-MAY-2005;
        Rockefeller University; New York, NY
FEATURES
    source
        location/Qualifiers
            1..27
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN

Query Match      65.3%; Score 12.4; DB 2; Length 27;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db  19 GGAGAAGGTGGTGG 6

RESULT 27
LOCUS BD171352
DEFINITION Method for predicting sensitivity to Helicobacter Pylori by
        analysis of gene polymorphism of secretion type gene, Lewis gene,
        interleukin 1B and myeloperoxidase gene.
ACCESSION BD171352
VERSION BD171352.1 GI:28412642
KEYWORDS JP 2002218996-A/5.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hamajima,N., Ikehara,Y., Tatematsu,M. and Nishibara,S.
TITLE Method for predicting sensitivity to Helicobacter Pylori by
        analysis of gene polymorphism of secretion type gene, Lewis gene,
        interleukin 1B and myeloperoxidase gene
JOURNAL Patent: JP 2002218996-A 5 06-AUG-2002;
        NOBUYUKI HAMAJIMA,YUZURU IKEHARA,MASAMORI TATEMATSU,SHOKO NISHIHARA
COMMENT PN JP 2002218996-A/5
        PD 06-AUG-2002
        PF 23-JAN-2001 JP 2001014871
        PI NOBUYUKI HAMAJIMA,YUZURU IKEHARA,MASAMORI TATEMATSU,SHOKO NISHIHARA
        PC C12Q1/68,C12N15/09,C12N15/00
        CC Method for predicting sensitivity to Helicobacter Pylori by
        CC analysis of
        CC gene polymorphism of secretion type gene, Lewis gene, CC
        CC interleukin 1B and
        CC myeloperoxidase gene
        FH Key Location/Qualifiers
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FT source 1..30
/organism="Unidentified".
FEATURES
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        location/Qualifiers
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                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
ORIGIN

Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4 GAAGGGGGTGGGTG 17
    ||||| |||||
Db  5 GCAGGGGGTGGGTG 18

RESULT 28
LOCUS I26957
DEFINITION Sequence 6 from patent US 5561224.
ACCESSION I26957
VERSION I26957.1 GI:1606827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Rosenfeld,M.G. and Anderson,B.
TITLE Transcription factor for regulation of the development of skin and
        hair
JOURNAL Patent: US 5561224-A 6 01-OCT-1996;
FEATURES
    source
        location/Qualifiers
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                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN

Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db  24 GGAGAAGGAGGTGG 11

RESULT 29
LOCUS AR306619/c
DEFINITION Sequence 10 from patent US 6548642.
ACCESSION AR306619
VERSION AR306619.1 GI:31696821
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 10 15-APR-2003;
        Ohio University; Athens, OH
FEATURES
    source
        location/Qualifiers
            1..30
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN

Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 30
LOCUS AR306628/c
DEFINITION Sequence 38 from patent US 6548642.
ACCESSION AR306628
VERSION AR306628.1 GI:31696830
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 38 15-APR-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 31
LOCUS AR306629
DEFINITION Sequence 39 from patent US 6548642.
ACCESSION AR306629
VERSION AR306629.1 GI:31696831
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums
JOURNAL Patent: US 6548642-A 39 15-APR-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 32
LOCUS AR340054/c
DEFINITION Sequence 10 from patent US 6570062.
ACCESSION AR340054
VERSION AR340054.1 GI:33731348
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
JOURNAL Patent: US 6570062-A 39 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="unassigned DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 33
LOCUS AR340063/c
DEFINITION Sequence 38 from patent US 6570062.
ACCESSION AR340063
VERSION AR340063.1 GI:33731357
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
JOURNAL Patent: US 6570062-A 38 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="unassigned DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 34
LOCUS AR340064
DEFINITION Sequence 39 from patent US 6570062.
ACCESSION AR340064
VERSION AR340064.1 GI:33731358
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
JOURNAL Patent: US 6570062-A 39 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="unassigned DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
Db 29 GGAGATGGGGTGG 16

RESULT 35
LOCUS AR340065/c
DEFINITION Sequence 38 from patent US 6570062.
ACCESSION AR340065
VERSION AR340065.1 GI:33731359
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kieliszewski,M.J.
TITLE Synthetic genes for plant gums and other hydroxyproline-rich
JOURNAL Patent: US 6570062-A 38 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..30
/mol_type="unassigned DNA"

ORIGIN
Query Match 65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGG 14
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGG 14
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Db 11 GGAGATGGGGTGG 24

RESULT 35
AR412123/c
LOCUS      AR412123      30 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 10 from patent US 6639050.
ACCESSION  AR412123
VERSION     AR412123.1 GI:40166767
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Kieliszewski,M.J.
TITLE      Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL    Patent: US 6639050-A 10 28-OCT-2003;
           Ohio University; Athens, OH
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGG 14
    ||||| ||||| |||||
Db 29 GGAGATGGGGTGG 16

RESULT 36
AR412132/c
LOCUS      AR412132      30 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6639050.
ACCESSION  AR412132
VERSION     AR412132.1 GI:40166776
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Kieliszewski,M.J.
TITLE      Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL    Patent: US 6639050-A 38 28-OCT-2003;
           Ohio University; Athens, OH
FEATURES   Location/Qualifiers
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Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
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Qy 1 GGAGAAGGGGTGG 14
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Db 29 GGAGATGGGGTGG 16

RESULT 37
AR412133
LOCUS      AR412133      30 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 39 from patent US 6639050.
ACCESSION  AR412133
VERSION     AR412133.1 GI:40166777
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Kieliszewski,M.J.
TITLE      Synthetic genes for plant gums and other hydroxyproline-rich
glycoproteins
JOURNAL    Patent: US 6639050-A 39 28-OCT-2003;
           Ohio University; Athens, OH
FEATURES   Location/Qualifiers
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Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2e+05;
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Qy 1 GGAGAAGGGGTGG 14
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Db 11 GGAGATGGGGTGG 24

RESULT 38
AR782390
LOCUS      AX782390      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Sequence 721 from Patent WO03050284.
ACCESSION  AX782390
VERSION     AX782390.1 GI:32950239
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Guo,J.
TITLE      Human prostate cancer candidate protein 1
JOURNAL    Patent: WO 03050284-A 721 19-JUN-2003;
           Amersham Biosciences (SV) Corp. (US)
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Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGTGGT 17
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Db 1 GGAGAAGGGGTGGTGGT 17

RESULT 39
AR016234/c
LOCUS      AR016234      18 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 122 from patent US 5776682.
ACCESSION  AR016234
VERSION     AR016234.1 GI:3972511
KEYWORDS   .
SOURCE     Unknown.
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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS First, M. Kent., Agoulnik, A.I., and Muallem, A.
TITLE Male infertility Y-deletion detection battery
JOURNAL Patent: US 5776682-A 122 07-JUL-1998;
FEATURES Location/Qualifiers
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Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTG 17
Db 18 GAAGAAGGGGTGGGTG 2

RESULT 40
LOCUS AR035649
DEFINITION Sequence 81 from patent US 5871920.
ACCESSION AR035649
VERSION AR035649.1 GI:5952317
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Page, D.C. and Reijo, R.
TITLE Daz: a gene associated with azoospermia
JOURNAL Patent: US 5871920-A 81 16-FEB-1999;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 2.4e+05;
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Qy 1 GGAGAAGGGGTGGGTG 17
Db 18 GAAGAAGGGGTGGGTG 2

RESULT 41
LOCUS AR060627
DEFINITION Sequence 10 from patent US 5840708.
ACCESSION AR060627
VERSION AR060627.1 GI:5987077
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weiss, B.
TITLE Administration of oligonucleotides antisense to dopamine receptor
JOURNAL MRNA for diagnosis and treatment of Neurological pathologies
FEATURES Patent: US 5840708-A 10 24-NOV-1998;
source
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ORIGIN

Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTG 17
Db 17 GGAGATGGAGGTAGGTG 1

RESULT 42
LOCUS CQ786920
DEFINITION Sequence 97 from Patent WO2004021010.
ACCESSION CQ786920
VERSION CQ786920.1 GI:45721912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nakamura, Y. and Furukawa, Y.
TITLE Method of diagnosing colon and gastric cancers
JOURNAL Patent: WO 2004021010-A 97 11-MAR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the president of the university of Tokyo (JP)

FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="Artificially synthesized primer sequence for RT-PCR"

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Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGGTGCT 19
Db 18 AGAAGGGGTGGGGCCT 2

RESULT 43
LOCUS CQ800189
DEFINITION Sequence 14 from Patent WO2004031411.
ACCESSION CQ800189
VERSION CQ800189.1 GI:46849107
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nakamura, Y. and Katagiri, T.
TITLE Genes and polypeptides relating to human pancreatic cancers
JOURNAL Patent: WO 2004031411-A 14 15-APR-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by The president of the University of Tokyo (JP)

FEATURES Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGGTGCT 19
Db 18 AGAAGGGGTGGGGCCT 2

RESULT 44
CQ875013/c
LOCUS CQ875013 linear PAT 27-SEP-2004
DEFINITION Sequence 35 from Patent WO2004076623.
ACCESSION CQ875013
VERSION CQ875013.1 GI:52748106
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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Db 18 AGAAGGAGGTGGGGCCT 2

RESULT 45
CS012032/c
LOCUS CS012032 linear PAT 11-FEB-2005
DEFINITION Sequence 1957 from Patent WO2005007144.
ACCESSION CS012032
VERSION CS012032.1 GI:59671847
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AUTHORS
TITLE
JOURNAL
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 18 ACAAGTGGGTGGGTGCT 2

RESULT 46
CS163806/c
LOCUS CS163806 linear PAT 26-SEP-2005
DEFINITION Sequence 17 from Patent WO2005083086.

ACCESSION CS163806
VERSION CS163806.1 GI:76360380
KEYWORDS
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AUTHORS
TITLE
JOURNAL
FEATURES
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/note="An artificially synthesized primer sequence"

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Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 AGAAGGGGGTGGGTGCT 19
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Db 18 AGAAGGAGGTGGGGCCT 2

RESULT 47
CS174584/c
LOCUS CS174584 linear PAT 12-OCT-2005
DEFINITION Sequence 15 from Patent WO2005090398.
ACCESSION CS174584
VERSION CS174584.1 GI:77625448
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REFERENCE
AUTHORS
TITLE
JOURNAL
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/db_xref="taxon:32630"
/note="An artificially synthesized primer sequence"

ORIGIN
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Best Local Similarity 82.4%; Pred. No. 2.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3 AGAAGGGGGTGGGTGCT 19
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Db 18 AGAAGGAGGTGGGGCCT 2

RESULT 48
CS174749/c
LOCUS CS174749 linear PAT 12-OCT-2005
DEFINITION Sequence 28 from Patent WO2005090572.
ACCESSION CS174749
VERSION CS174749.1 GI:77625601
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Compositions and methods for treating pancreatic cancer

JOURNAL Patent: WO 2005090572-A 28 29-SEP-2005;
The University of Tokyo (JP); Oncotherapy Science, Inc. (JP)
FEATURES
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Db 18 AGAAGGAGGTGGGCCT 2
RESULT 49
AR315974/c
LOCUS AR315974 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6511 from patent US 6559294.
ACCESSION AR315974
VERSION AR315974.1 GI:31709400
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6511 06-MAY-2003;
Genset, S.A.;
FRX;
FEATURES
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Best Local Similarity 82.4%; Pred. NO. 2.5e+05;
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Qy 2 GAGAGGGGTGGGTGC 18
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Db 19 GAGAAGGGGTAGGAGC 3
RESULT 50
AR565351/c
LOCUS AR565351 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 29 from patent US 6767705.
ACCESSION AR565351
VERSION AR565351.1 GI:53981207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Roninson, I.B., Dokmanovic, M. and Chang, B.-D.
TITLE Reagents and methods for identifying and modulating expression of
genes regulated by retinoids
JOURNAL Patent: US 6767705-A 29 27-JUL-2004;
The Board of Trustees of the University of Illinois; Urbana, IL
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Qy 1 GGAGNAGGGGTGGGTG 17
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Db 19 GAAGAAGGGGGAGGATG 3
Search completed: October 14, 2006, 20:12:31
Job time : 2043 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:34:51 ; Search time 300 Seconds

(without alignments)
441.576 Million cell updates/sec

Title: US-10-604-926A-4539

Perfect score: 19

Sequence: 1 ggagaagggtgggtgct 19

Scoring table: IDENTIFY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 4443654

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : N_Geneseq.8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
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- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

'Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	77.9	22	10	Adf17589 Beta A PC
2	14.2	74.7	26	8	Abx10197 S. aggreg
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C 4	13.8	72.6	20	2	Aat86507 S-adenosy
5	13.8	72.6	20	13	Adk23254 Acyl-coen
6	13.8	72.6	20	13	Adk23371 Acyl-coen
7	13.8	72.6	20	13	Adk23372 Acyl-coen
8	13.8	72.6	20	13	Adk23389 Acyl-coen
C 9	13.8	72.6	20	15	Aef42976 Mesoblast
C 10	13.8	72.6	21	12	Adn00574 Murine ad
C 11	13.8	72.6	21	14	Ady38715 Mouse adi
C 12	13.8	72.6	23	14	Adw43979 Human MOD
C 13	13.4	70.5	19	14	Adz87881 Early gro
C 14	13.4	70.5	19	14	Adz88055 Early gro
15	13.4	70.5	19	14	Aeb43635 Novel hum
C 16	13.4	70.5	19	14	Aeb43461 Novel hum
C 17	13.4	70.5	22	6	Aad45780 Human pro
C 18	13.2	69.5	18	3	Aaz75471 Human bia

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c 93	12.4	65.3	30	6	ABL51739	Ab151739 Hydroxypr	166	12	63.2	22	15	AEF05498	Aef05498 Bisulfite
c 94	12.4	65.3	30	6	ABL51740	Ab151740 Hydroxypr	167	12	63.2	20	4	AAS95201	Aas95201 Otoferrin
c 95	12.4	65.3	30	13	ADU09143	Adu09143 Ser-Hyp4	c 168	11.8	62.1	15	2	AAQ93299	Aaq93299 Multi-dru
c 96	12.4	65.3	30	13	ADU09116	Adu09116 Hydroxypr	c 169	11.8	62.1	17	5	ADV03315	Adv03315 Human BAC
c 97	12.4	65.3	30	13	ADU09144	Adu09144 Ser-Hyp4	c 170	11.8	62.1	17	5	ADV02233	Adv02233 Human BAC
c 98	12.2	64.2	17	10	ADF62817	Adf62817 Human PCC	c 171	11.8	62.1	17	5	ADV03316	Adv03316 Human BAC
c 99	12.2	64.2	18	2	AA768368	Aat68368 Loc1-spec	c 172	11.8	62.1	17	6	ABN06799	Abn06799 Human GDM
c 100	12.2	64.2	18	2	AAx01506	Aax01506 Primer ST	c 173	11.8	62.1	17	6	ABN06800	Abn06800 Human GDM
c 101	12.2	64.2	18	3	AA292565	Aa292565 Human Y-s	c 174	11.8	62.1	17	6	ABN06798	Abn06798 Human GDM
c 102	12.2	64.2	18	13	ADT01610	Adt01610 Novel mut	c 175	11.8	62.1	17	13	ACN69889	Acn69889 Human GDM
c 103	12.2	64.2	19	10	ADD68684	Ad68684 DNA ampli	c 176	11.8	62.1	17	13	ACN69890	Acn69890 Human GDM
c 104	12.2	64.2	20	2	AAQ68205	Aaq68205 Human D2	c 177	11.8	62.1	17	13	ACN69888	Acn69888 Human GDM
c 105	12.2	64.2	20	2	AA786561	Aat86561 Human D2	c 178	11.8	62.1	18	5	AAS43549	Aas43549 Corneodes
c 106	12.2	64.2	20	2	AAx97185	Aax97185 Primer us	c 179	11.8	62.1	18	5	ADL18253	Adl18253 Antisense
c 107	12.2	64.2	20	5	AA522302	Aas22302 Human COL	c 180	11.8	62.1	19	2	AAx56945	Aax56945 HIV-1 pro
c 108	12.2	64.2	20	5	AA522301	Aas22301 Human COL	c 181	11.8	62.1	19	14	AEA42783	Aea42783 Human WNT
c 109	12.2	64.2	20	6	AD24940	Ad24940 Antisense	c 182	11.8	62.1	19	14	AEA42620	Aea42620 Human WNT
c 110	12.2	64.2	20	10	ABZ87731	Abz87731 Human oli	c 183	11.8	62.1	19	14	AEC25862	Aec25862 Human all
c 111	12.2	64.2	20	11	ABD23961	Abd23961 Human cal	c 184	11.8	62.1	19	14	AEC28228	Aec28228 Human all
c 112	12.2	64.2	20	12	ADL64441	Adl64441 Human U6s	c 185	11.8	62.1	19	15	AEE65444	Aee65444 Human vit
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c 115	12.2	64.2	20	13	ADW87729	Adw87729 Genomic D	c 188	11.8	62.1	20	4	RAH23483	Rah23483 Human dop
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c 118	12.2	64.2	20	14	AED14984	Aed14984 Human snR	c 191	11.8	62.1	20	13	ADK23468	Adk23468 Acyl-coen
c 119	12.2	64.2	20	14	AED17711	Aed17711 Human snR	c 192	11.8	62.1	20	14	ADW44009	Adw44009 Human MOD
c 120	12.2	64.2	20	15	AEE63417	Aee63417 Human snR	c 193	11.8	62.1	20	15	AEE78274	Aee78274 Human dop
c 121	12.2	64.2	20	15	ABF74439	Aef74439 Human snR	c 194	11.8	62.1	20	15	AEE78276	Aee78276 Human dop
c 122	12.2	64.2	21	6	ABS66907	Abs66907 Human MRP	c 195	11.8	62.1	20	15	AEE78272	Aee78272 Human dop
c 123	12.2	64.2	21	6	ABS66906	Abs66906 Human MRP	c 196	11.8	62.1	20	15	AEE78277	Aee78277 Human dop
c 124	12.2	64.2	21	8	AD49478	Ad49478 Second PC	c 197	11.8	62.1	20	15	AEE78273	Aee78273 Human dop
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c 126	12.2	64.2	21	14	ADZ25719	Adz25719 HIV-1 Tat	c 199	11.8	62.1	21	2	AAT64846	Aat64846 CMV immed
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c 128	12.2	64.2	21	14	AEC26551	Aec26551 Human all	c 201	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
c 129	12.2	64.2	22	2	AAT11034	Aat11034 Antisense	c 202	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
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c 132	12.2	64.2	22	4	AAF58876	Aaf58876 Human met	c 205	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
c 133	12.2	64.2	22	4	AAF58876	Aaf58876 Human met	c 206	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
c 134	12.2	64.2	22	4	AAF58878	Aaf58878 Human met	c 207	11.8	62.1	21	4	RAH41879	Rah41879 Cytomegal
c 135	12.2	64.2	22	13	ADS19194	Adsl9194 MHC class	c 208	11.8	62.1	22	2	AAx22539	Aax22539 Human MMP
c 136	12.2	64.2	23	2	AAV60613	Aav60613 PCR prime	c 209	11.8	62.1	22	2	AAx22539	Aax22539 Human MMP
c 137	12.2	64.2	23	14	ADW08913	Adw08913 Canine be	c 210	11.8	62.1	22	10	ADF94328	Adf94328 Murine neu
c 138	12.2	64.2	24	6	ABN74968	Abn74968 Human MNR	c 211	11.8	62.1	23	4	ABH74156	Aah74156 Human neu
c 139	12.2	64.2	25	10	ADF63568	Adf63568 Human PCC	c 212	11.8	62.1	23	4	ABH74156	Aah74156 Human neu
c 140	12.2	64.2	25	10	ADF63566	Adf63566 Human PCC	c 213	11.8	62.1	24	2	AAV09032	Aav09032 Human Na+
c 141	12.2	64.2	25	10	ADF63562	Adf63562 Human PCC	c 214	11.8	62.1	24	2	AAV09032	Aav09032 Human Na+
c 142	12.2	64.2	25	10	ADF63567	Adf63567 Human PCC	c 215	11.8	62.1	24	6	ABQ02013	Abq02013 Imperfect
c 143	12.2	64.2	25	10	ADF63561	Adf63561 Human PCC	c 216	11.8	62.1	24	6	ABQ02013	Abq02013 Imperfect
c 144	12.2	64.2	25	10	ADF63564	Adf63564 Human PCC	c 217	11.8	62.1	24	6	ABQ07946	Abq07946 Oligonuc1
c 145	12.2	64.2	25	10	ADF63565	Adf63565 Human PCC	c 218	11.8	62.1	24	6	ABQ07946	Abq07946 Oligonuc1
c 146	12.2	64.2	25	10	ADF63560	Adf63560 Human PCC	c 219	11.8	62.1	24	6	ABQ07987	Abq07987 Oligonuc1
c 147	12.2	64.2	25	10	ADF63563	Adf63563 Human PCC	c 220	11.8	62.1	24	6	ABQ07987	Abq07987 Oligonuc1
c 148	12.2	64.2	26	2	AA760163	Aat60163 Collagen	c 221	11.8	62.1	24	13	ADT78185	Adt78185 Human D2
c 149	12.2	64.2	26	2	AAx77401	Aax77401 Human tel	c 222	11.8	62.1	25	6	ABN11693	Abn11693 Human GDM
c 150	12.2	64.2	26	3	AAZ98711	Aaz98711 Collagen	c 223	11.8	62.1	25	6	ABN11693	Abn11693 Human GDM
c 151	12.2	64.2	27	12	ADJ14687	Adj14687 Debrisoqu	c 224	11.8	62.1	25	6	ABN11694	Abn11694 Human GDM
c 152	12.2	64.2	27	12	ADO60789	Ado60789 Human deb	c 225	11.8	62.1	25	6	ABN11694	Abn11694 Human GDM
c 153	12.2	64.2	27	14	AEC89953	Aec89953 CYP2D6 ge	c 226	11.8	62.1	25	6	ABN11695	Abn11695 Human GDM
c 154	12.2	64.2	29	3	AA04666	Aaa04666 Polymorph	c 227	11.8	62.1	25	6	ABN11695	Abn11695 Human GDM
c 155	12.2	64.2	29	9	ACC85464	Acc85464 T thermoh	c 228	11.8	62.1	25	6	ABN11699	Abn11699 Human GDM
c 156	12.2	64.2	30	2	AAQ89021	Aaq89021 VEGF 2'-N	c 229	11.8	62.1	25	6	ABN11700	Abn11700 Human GDM
c 157	12.2	64.2	30	6	AA223112	Aa223112 Human CD4	c 230	11.8	62.1	25	6	ABN11700	Abn11700 Human GDM
c 158	12.2	64.2	30	6	AA141207	Aa141207 HIV-1 env	c 231	11.8	62.1	25	6	ABN11690	Abn11690 Human GDM
c 159	12.2	64.2	30	7	ADY31410	Ady31410 Human CDC	c 232	11.8	62.1	25	6	ABN11692	Abn11692 Human GDM
c 160	12.2	64.2	30	7	ADY36798	Ady36798 CDC2l1 fo	c 233	11.8	62.1	25	6	ABN11698	Abn11698 Human GDM
c 161	12.2	64.2	30	9	ACC85466	Acc85466 T thermoh	c 234	11.8	62.1	25	6	ABN11697	Abn11697 Human GDM
c 162	12.2	63.2	15	6	ABA96072	Ab96072 PCR prime	c 235	11.8	62.1	25	6	ABN11691	Abn11691 Human GDM
c 163	12.2	63.2	17	3	AAF06236	Aaf06236 Hammerhea	c 236	11.8	62.1	25	6	ABN11691	Abn11691 Human GDM
c 164	12.2	63.2	20	10	ADD20323	Add20323 Oreochrom	c 237	11.8	62.1	25	13	ACN74781	Acn74781 Human GDM

238	11.8	62.1	25	13	ACN74784	Acn74784 Human GDM	C 311	11.6	61.1	21	13	ADT88487	Adt88487 Vasoactiv
239	11.8	62.1	25	13	ACN74786	Acn74786 Human GDM	C 312	11.6	61.1	21	14	ADZ87553	Adz87553 DNA methy
240	11.8	62.1	25	13	ADT99600	Adt99600 Quadruple	C 313	11.6	61.1	21	14	ADZ77235	Adz77235 Reverse p
241	11.8	62.1	25	13	ADT92593	Adt92593 Quadruple	C 314	11.6	61.1	21	15	AEF40164	Aef40164 Dengue vi
C 242	11.8	62.1	26	2	AAQ99939	AAQ99939 Mouse WTS	C 315	11.6	61.1	22	2	AAQ01725	AAQ01725 Human typ
C 243	11.8	62.1	26	2	AAQ00732	AAQ00732 Multiple	C 316	11.6	61.1	22	10	ADJ33160	Adj33160 Primer se
C 244	11.8	62.1	26	2	AAV72306	AAV72306 P16 promo	C 317	11.6	61.1	23	5	AAF62511	Aaf62511 CDKN2A ex
C 245	11.8	62.1	26	2	AAV53846	AAV53846 Nucleotid	C 318	11.6	61.1	23	10	ADQ67683	Adq67683 Pfiesteri
C 246	11.8	62.1	26	2	AAV11265	AAV11265 Human MTS	C 319	11.6	61.1	24	4	AAI65243	Aai65243 Human pro
C 247	11.8	62.1	26	2	AAV40771	AAV40771 Oligonuc	C 320	11.6	61.1	24	6	ABK91194	Abk91194 Human pri
C 248	11.8	62.1	26	2	AAV70610	AAV70610 Probe use	C 321	11.6	61.1	24	6	ABS56309	Abs56309 Rice chro
C 249	11.8	62.1	26	2	AAQ95558	AAQ95558 Mouse P16	C 322	11.6	61.1	24	10	ADH16989	Adh16989 Mouse mon
C 250	11.8	62.1	26	3	AAQ95247	AAQ95247 Zea mays	C 323	11.6	61.1	24	12	ADO10733	Ado10733 Single mu
C 251	11.8	62.1	26	3	AAZ48797	AAZ48797 PCR prime	C 324	11.6	61.1	24	12	ADO10785	Ado10785 Single mu
C 252	11.8	62.1	26	3	AAZ39996	AAZ39996 PCR prime	C 325	11.6	61.1	24	12	ADQ09925	Adq09925 Mouse RT-
C 253	11.8	62.1	26	3	AAQ39380	AAQ39380 Mouse P16	C 326	11.6	61.1	24	14	ADM22719	Adm22719 Transposo
C 254	11.8	62.1	26	3	AAQ11190	AAQ11190 Mouse mul	C 327	11.6	61.1	24	14	ADY72807	Ady72807 Neomycin
C 255	11.8	62.1	26	4	AAQ58198	AAQ58198 Oligonuc	C 328	11.6	61.1	25	2	AAQ35207	Aaq35207 Neomycin
C 256	11.8	62.1	26	4	AAQ02591	AAQ02591 PCR prime	C 329	11.6	61.1	25	2	AAQ16986	Aaq16986 Primer #2
C 257	11.8	62.1	26	4	AAQ04739	AAQ04739 Alternati	C 330	11.6	61.1	25	9	ACI37385	Act37385 Human mlc
C 258	11.8	62.1	26	4	AAQ83098	AAQ83098 Biotinyla	C 331	11.6	61.1	25	9	ACI77545	Act77545 Human mlc
C 259	11.8	62.1	26	13	ADZ15717	Adz15717 Mutagenic	C 332	11.6	61.1	25	9	ACC84797	Acc84797 Nucleotid
C 260	11.8	62.1	27	2	AAQ95879	AAQ95879 Competito	C 333	11.6	61.1	25	10	AAQ55668	Aaq55668 Bovine vi
C 261	11.8	62.1	27	4	AAQ21692	AAQ21692 Imperfect	C 334	11.6	61.1	26	12	ADL23290	Adl23290 GMCSF-Gas
C 262	11.8	62.1	27	4	AAQ21705	AAQ21705 Imperfect	C 335	11.6	61.1	27	6	ABS66909	Abs66909 Human MRP
C 263	11.8	62.1	27	4	AAQ21702	AAQ21702 Imperfect	C 336	11.6	61.1	27	6	ABS66908	Abs66908 Human MRP
C 264	11.8	62.1	27	4	AAQ21699	AAQ21699 Imperfect	C 337	11.6	61.1	27	6	ABS68769	Abs68769 Archaeogl
C 265	11.8	62.1	28	2	AAQ31105	AAQ31105 Probe 74	C 338	11.6	61.1	27	8	ADE53128	Ade53128 PEN-1 rel
C 266	11.8	62.1	28	6	AAQ35016	AAQ35016 Mismatche	C 339	11.6	61.1	27	8	ACF62504	Act62504 Cancer ba
C 267	11.8	62.1	28	9	ADA01886	Ada01886 Mouse car	C 340	11.6	61.1	27	8	ADB21175	Adb21175 MRP1 base
C 268	11.8	62.1	28	10	ADH71625	Adh71625 Mouse car	C 341	11.6	61.1	27	10	ADB88264	Adb88264 Human UGT
C 269	11.8	62.1	28	12	ADH23328	Adh23328 Human GAT	C 342	11.6	61.1	27	10	ADB97247	Adb97247 Human MRP
C 270	11.8	62.1	29	3	AAQ3284	AAQ3284 H. vulgar	C 343	11.6	61.1	27	10	ADB92438	Adb92438 Human MRP
C 271	11.8	62.1	30	4	AAH91290	AAH91290 Human inf	C 344	11.6	61.1	27	14	ABE87355	AbE87355 Archaeogl
C 272	11.6	61.1	18	6	ABT04100	ABT04100 Human VEG	C 345	11.6	61.1	27	14	AEC76623	Aec76623 Maize Bra
C 273	11.6	61.1	18	8	ACD06057	ACD06057 Human VEG	C 346	11.6	61.1	27	14	AEC76625	Aec76625 Maize Bra
C 274	11.6	61.1	18	9	ACD19279	ACD19279 Human VEG	C 347	11.6	61.1	27	14	AEC76624	Aec76624 Maize Bra
C 275	11.6	61.1	18	14	AEC51722	Aec51722 Antisense	C 348	11.6	61.1	27	14	AEC76622	Aec76622 Maize Bra
C 276	11.6	61.1	18	14	AED55570	Aed55570 Human VEG	C 349	11.6	61.1	28	10	ADK71330	Adk71330 Drug-tole
C 277	11.6	61.1	18	15	AEE10252	Aee10252 Human VEG	C 350	11.6	61.1	28	14	AEC36488	Aec36488 Multifunc
C 278	11.6	61.1	19	2	AAZ06728	AAZ06728 Antisense	C 351	11.6	61.1	28	14	AEC36526	Aec36526 Probe for
C 279	11.6	61.1	19	3	AAZ60424	AAZ60424 PCR prime	C 352	11.6	61.1	29	2	AAV58366	Aav58366 Secondary
C 280	11.6	61.1	19	3	AAZ37936	AAZ37936 Adenovira	C 353	11.6	61.1	29	12	ADL23301	Adl23301 GM-CSF up
C 281	11.6	61.1	19	3	AAQ91780	AAQ91780 Inhibin B	C 354	11.6	61.1	29	12	ADL23301	Adl23301 GM-CSF up
C 282	11.6	61.1	19	5	AAQ88825	AAQ88825 Ad5 hexon	C 355	11.6	61.1	30	13	ADV25245	Adv25245 Rice rubi
C 283	11.6	61.1	19	10	ADE27501	Ade27501 Stearoyl-	C 356	11.6	61.1	30	14	AEA28546	Aea28546 nptii tra
C 284	11.6	61.1	19	10	ADE27211	Ade27211 Stearoyl-	C 357	11.6	61.1	30	14	AEI58912	Aei58912 Human ost
C 285	11.6	61.1	19	14	ADZ20451	Adz20451 Adenoviru	C 358	11.6	61.1	30	14	AEI59921	Aei59921 Primer rd
C 286	11.6	61.1	19	14	ABE08591	AbE08591 Human ade	C 359	11.4	60.0	13	5	ABC22094	Abc22094 Oligonuc
C 287	11.6	61.1	19	14	AED58639	Aed58639 Human ost	C 360	11.4	60.0	13	5	ABC81987	Abc81987 Oligonuc
C 288	11.6	61.1	19	14	AED52176	Aed52176 Human SCD	C 361	11.4	60.0	13	5	ABC34318	Abc34318 Oligonuc
C 289	11.6	61.1	19	14	AED51886	Aed51886 Human SCD	C 362	11.4	60.0	13	5	ABC22095	Abc22095 Oligonuc
C 290	11.6	61.1	19	14	AEE53337	Aee53337 Human hai	C 363	11.4	60.0	13	5	ABC81986	Abc81986 Oligonuc
C 291	11.6	61.1	19	14	AEE53336	Aee53336 Human hai	C 364	11.4	60.0	13	5	ABC34319	Abc34319 Oligonuc
C 292	11.6	61.1	19	14	AEE53339	Aee53339 Human hai	C 365	11.4	60.0	13	5	ABZ10378	Abz10378 Haematopo
C 293	11.6	61.1	19	14	AEE53338	Aee53338 Human hai	C 366	11.4	60.0	13	12	ADM76188	Adm76188 NEPHA gen
C 294	11.6	61.1	20	2	AAQ82424	AAQ82424 Chromosom	C 367	11.4	60.0	14	6	ABQ73006	Abq73006 Human liv
C 295	11.6	61.1	20	2	AAQ32535	AAQ32535 Primer fo	C 368	11.4	60.0	14	12	ADM76189	Adm76189 NEPHA gen
C 296	11.6	61.1	20	3	AAQ11329	AAQ11329 Human TRP	C 369	11.4	60.0	15	4	AAF46341	Aaf46341 IGFBP2 ol
C 297	11.6	61.1	20	5	AAQ17452	AAQ17452 Human TNF	C 370	11.4	60.0	15	4	AAF46340	Aaf46340 IGFBP2 ol
C 298	11.6	61.1	20	6	ABS53068	ABS53068 P75NTR ge	C 371	11.4	60.0	15	4	AAF46339	Aaf46339 IGFBP2 ol
C 299	11.6	61.1	20	8	ACC00618	Acc00618 Human CAP	C 372	11.4	60.0	15	6	AAQ99365	Aaq99365 Aldehyde
C 300	11.6	61.1	20	10	ADP88546	Adp88546 Single nu	C 373	11.4	60.0	17	3	AAQ70181	Aaq70181 Single nu
C 301	11.6	61.1	20	10	ADH48653	Adh48653 PCR prime	C 374	11.4	60.0	17	3	AAF02086	Aaf02086 Hammerhea
C 302	11.6	61.1	20	10	ADA66475	Ada66475 Transform	C 375	11.4	60.0	17	3	AAF02200	Aaf02200 Hammerhea
C 303	11.6	61.1	20	13	ADS73957	Ads73957 Human TNF	C 376	11.4	60.0	17	3	AAF02085	Aaf02085 Hammerhea
C 304	11.6	61.1	20	13	ADT00840	Adt00840 Novel mut	C 377	11.4	60.0	17	4	AAF60104	Aaf60104 Human ATM
C 305	11.6	61.1	21	6	ABS66905	Abs66905 Human MRP	C 378	11.4	60.0	17	5	ADV02092	Adv02092 Human TER
C 306	11.6	61.1	21	6	ABS66904	Abs66904 Human MRP	C 379	11.4	60.0	17	6	ABL55546	AbL55546 Oligonuc
C 307	11.6	61.1	21	11	ADJ13140	Adj13140 Human DNA	C 380	11.4	60.0	17	6	ABL55545	AbL55545 Oligonuc
C 308	11.6	61.1	21	11	ADJ13105	Adj13105 Human DNA	C 381	11.4	60.0	17	6	ABV78976	Abv78976 Human HTP
C 309	11.6	61.1	21	12	ADO25173	Ado25173 MCAM mRNA	C 382	11.4	60.0	17	6	ABV78972	Abv78972 Human HTP
C 310	11.6	61.1	21	13	ADR47012	Adr47012 Dengue vi	C 383	11.4	60.0	17	6	ABV78974	Abv78974 Human HTP

C 384	11.4	60.0	17	6	ABV78973	Abv78973 Human HTP	C 457	11.4	60.0	24	10	ADC68835	Adc68835 Human PRO
C 385	11.4	60.0	17	6	ABV78975	Abv78975 Human HTP	C 458	11.4	60.0	24	10	ADC62895	Adc62895 Human PRO
C 386	11.4	60.0	17	12	ADP03206	Adp03206 Allele sp	C 459	11.4	60.0	24	10	ADC67960	Adc67960 Human PRO
C 387	11.4	60.0	17	15	AEF55485	Aef55485 Human gen	C 460	11.4	60.0	24	10	ADCA1280	Adca1280 Human PRO
C 388	11.4	60.0	18	6	AAH74510	Aah74510 PCR prime	C 461	11.4	60.0	24	10	ADC67335	Adc67335 Human PRO
C 389	11.4	60.0	18	6	ABL45137	Abl45137 Human chr	C 462	11.4	60.0	24	10	ADC62271	Adc62271 Human PRO
C 390	11.4	60.0	19	6	ABQ74948	Aeq74948 Medane re	C 463	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 391	11.4	60.0	19	9	ACH66546	Ach66546 Antisense	C 464	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 392	11.4	60.0	19	13	ADR12295	Adr12295 15-lipox	C 465	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 393	11.4	60.0	19	13	ADR75668	Adr75668 Human apo	C 466	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 394	11.4	60.0	19	13	ADR78286	Adr78286 Human apo	C 467	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 395	11.4	60.0	19	13	ADT82729	Adt82729 Apolipop	C 468	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 396	11.4	60.0	19	13	ADT80111	Adt80111 Apolipop	C 469	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 397	11.4	60.0	19	14	AEBS0994	Aeb50994 Human ADA	C 470	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 398	11.4	60.0	19	14	AEBS0798	Aeb50798 Human ADA	C 471	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 399	11.4	60.0	20	2	AAQ92082	Aaq92082 Erythro	C 472	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 400	11.4	60.0	20	2	AAQ74112	Aaq74112 Human ery	C 473	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 401	11.4	60.0	20	2	AAQ96882	Aaq96882 PCR prime	C 474	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 402	11.4	60.0	20	2	AAQ96879	Aaq96879 PCR prime	C 475	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 403	11.4	60.0	20	3	AAQ98282	Aaq98282 Human MSH	C 476	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 404	11.4	60.0	20	6	ABK14871	Abk14871 Human TCF	C 477	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 405	11.4	60.0	20	10	ADE94296	Ade94296 Human Epo	C 478	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 406	11.4	60.0	20	10	ABZ84914	Abz84914 Human oli	C 479	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 407	11.4	60.0	20	11	ABD21144	Abd21144 Human tra	C 480	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 408	11.4	60.0	20	12	ADQ78193	Adq78193 PCR prime	C 481	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 409	11.4	60.0	20	14	AEC25118	Aec25118 Human all	C 482	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 410	11.4	60.0	20	14	AEC27484	Aec27484 Human all	C 483	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 411	11.4	60.0	20	14	AED13220	Aed13220 Human PLJ	C 484	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 412	11.4	60.0	20	15	AEF23151	Aef23151 Protein t	C 485	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 413	11.4	60.0	21	6	ABK12845	Aab2576 Human alp	C 486	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 414	11.4	60.0	21	6	ABK12845	Abk12845 5' SST fo	C 487	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 415	11.4	60.0	21	11	ADJ13245	Adj13245 Human DNA	C 488	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 416	11.4	60.0	21	14	ADM97087	Adm97087 HbAFP CDN	C 489	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 417	11.4	60.0	22	2	AXX25642	Aax25642 EPO-fusio	C 490	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 418	11.4	60.0	22	2	AXX25703	Aax25703 Human ery	C 491	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 419	11.4	60.0	22	3	AAA49965	Aaa49965 Primer 13	C 492	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 420	11.4	60.0	22	4	AAI66680	Aai66680 Human CET	C 493	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 421	11.4	60.0	22	8	ADA00206	Ada00206 Mouse and	C 494	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 422	11.4	60.0	22	13	ADR83213	Adr83213 Human mir	C 495	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 423	11.4	60.0	22	13	ADR83367	Adr83367 Human Pax	C 496	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 424	11.4	60.0	22	14	ADX04735	Adx04735 Antisense	C 497	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 425	11.4	60.0	22	14	ADX04110	Adx04110 Human mat	C 498	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 426	11.4	60.0	22	14	ADY30955	Ady30955 Micro RNA	C 499	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 427	11.4	60.0	22	14	ABE79516	Abey79516 Human hsa	C 500	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 428	11.4	60.0	22	14	ABE79210	Abey79210 Human mic	C 501	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 429	11.4	60.0	22	14	AEC36268	Aec36268 Nucleotid	C 502	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 430	11.4	60.0	22	14	AED53439	Aed53439 Human tar	C 503	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 431	11.4	60.0	22	14	AEEO4350	Aee04350 Human mir	C 504	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 432	11.4	60.0	22	15	AEF60787	Aef60787 Mouse mic	C 505	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 433	11.4	60.0	23	2	AAH58191	Aah58191 Primer fo	C 506	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 434	11.4	60.0	23	4	AAH50124	Aah50124 Bacterial	C 507	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 435	11.4	60.0	23	10	ADF39467	Adf39467 HNRNP gen	C 508	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 436	11.4	60.0	23	12	ADQ98297	Adq98297 Primer of	C 509	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 437	11.4	60.0	24	2	AAQ88799	Aaq88799 Oligo PM3	C 510	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 438	11.4	60.0	24	3	AAZ34092	Aaz34092 Human PRO	C 511	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 439	11.4	60.0	24	3	AAZ58520	Aaz58520 Human PRO	C 512	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 440	11.4	60.0	24	3	AAZ78753	Aaz78753 Human PRO	C 513	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 441	11.4	60.0	24	3	AAZ49767	Aaz49767 Human PRO	C 514	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 442	11.4	60.0	24	3	AAZ61743	Aaz61743 Primer fo	C 515	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 443	11.4	60.0	24	8	ACA63660	Aca63660 Novel hum	C 516	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 444	11.4	60.0	24	8	ACA71824	Aca71824 Human PRO	C 517	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 445	11.4	60.0	24	8	ABX92464	Abx92464 Human PRO	C 518	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 446	11.4	60.0	24	8	ACN66205	Acn66205 Human sec	C 519	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 447	11.4	60.0	24	9	ADA24778	Ada24778 Secreted	C 520	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 448	11.4	60.0	24	9	ACD29806	Acd29806 Novel hum	C 521	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 449	11.4	60.0	24	9	ADA12439	Ada12439 Human sec	C 522	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 450	11.4	60.0	24	9	ACD29221	Acd29221 Novel hum	C 523	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 451	11.4	60.0	24	10	ADB73745	Adb73745 Human PRO	C 524	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 452	11.4	60.0	24	10	ADB76461	Adb76461 Human PRO	C 525	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 453	11.4	60.0	24	10	ADC43887	Adc43887 Human PRO	C 526	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 454	11.4	60.0	24	10	ADC61647	Adc61647 Human PRO	C 527	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 455	11.4	60.0	24	10	ADC63611	Adc63611 Human PRO	C 528	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO
C 456	11.4	60.0	24	10	ADC66711	Adc66711 Human PRO	C 529	11.4	60.0	24	10	ADCA1904	Adca1904 Human PRO

c 530	11.4	60.0	25	12	ADH72891	Adh72891 M. tuberc	603	11.2	58.9	19	14	AE55223	Human hai
c 531	11.4	60.0	25	12	ADP14600	Adp14600 Renal cel	604	11.2	58.9	19	14	AE55219	Human hai
c 532	11.4	60.0	25	13	ADR42656	Adr42656 Acetylase	c 605	11.2	58.9	19	14	AE55224	Human hai
c 533	11.4	60.0	25	13	ADR56507	Adr56507 Drug ther	c 606	11.2	58.9	19	15	AE65108	Human vit
c 534	11.4	60.0	26	2	AAV65661	Aav65661 Adenoviru	607	11.2	58.9	19	15	AE65364	Human vit
c 535	11.4	60.0	26	2	AAV57191	Aav57191 Porcine O	608	11.2	58.9	20	2	AAQ73373	Anti-HSV-
c 536	11.4	60.0	26	3	AAV58311	Aav58311 Human PRO	609	11.2	58.9	20	2	AAQ61986	AAQ61986 Inosine-s
c 537	11.4	60.0	26	13	ADU87192	Adu87192 B melanom	610	11.2	58.9	20	2	AAQ86840	Antisense
c 538	11.4	60.0	26	14	AE98383	Aeb98383 Rat GLUT3	611	11.2	58.9	20	2	AAQ86840	Antisense
c 539	11.4	60.0	26	14	AEC62733	Aec62733 Human 36B	612	11.2	58.9	20	2	AAQ86840	Antisense
c 540	11.4	60.0	27	8	ABV73361	Abv73361 Insect ce	c 613	11.2	58.9	20	2	AAQ86840	Antisense
c 541	11.4	60.0	27	10	AAV56130	Aal56130 EPO-Fc ex	614	11.2	58.9	20	2	AAQ86840	Antisense
c 542	11.4	60.0	27	12	ADU01527	Adu01527 Human EPO	615	11.2	58.9	20	2	AAQ86840	Antisense
c 543	11.4	60.0	27	12	ADP03174	Adp03174 Allele sp	c 616	11.2	58.9	20	3	AAQ86840	Antisense
c 544	11.4	60.0	27	14	ADV97101	Adv97101 PCR prime	c 617	11.2	58.9	20	3	AAQ86840	Antisense
c 545	11.4	60.0	28	2	AAV31811	Aav31811 Nucleotid	c 618	11.2	58.9	20	4	AAQ86840	Antisense
c 546	11.4	60.0	28	2	AAZ20722	Aaz20722 PCR prime	619	11.2	58.9	20	6	ABL58945	Human pro
c 547	11.4	60.0	28	3	AAZ60288	Aaz60288 Primer 7	c 620	11.2	58.9	20	9	ABZ71041	Human HXR
c 548	11.4	60.0	28	6	ABA93428	Ab93428 Aspergill	c 621	11.2	58.9	20	9	ACD05120	Tumour ne
c 549	11.4	60.0	28	13	ADT62023	Adt62023 Vector ps	c 622	11.2	58.9	20	10	ABZ87613	Human oli
c 550	11.4	60.0	29	3	AAA04352	Aaa04352 Polymorph	c 623	11.2	58.9	20	11	ABD23843	Human myo
c 551	11.4	60.0	29	4	AAQ09212	Aaq09212 PCR prime	c 624	11.2	58.9	20	12	ADK95473	Primer of
c 552	11.4	60.0	29	6	ADZ27411	Adz27411 Murine er	c 625	11.2	58.9	20	12	ADL57961	Human ESM
c 553	11.4	60.0	29	10	ADM13541	Adm13541 Mouse ery	c 626	11.2	58.9	20	12	ADL57961	Human ESM
c 554	11.4	60.0	29	11	ADM33836	Adm33836 Human ery	c 627	11.2	58.9	20	12	ADL57919	Human ESM
c 555	11.4	60.0	29	13	ADR48967	Adr48967 Human EPO	c 628	11.2	58.9	20	12	ADL57893	Human ESM
c 556	11.4	60.0	29	13	ADW47499	Adw47499 Human EPO	c 629	11.2	58.9	20	12	ADL57893	Human ESM
c 557	11.4	60.0	29	14	AEA18916	Aea18916 HuEPO-L-v	c 630	11.2	58.9	20	12	ADQ31326	Human XT-
c 558	11.4	60.0	29	14	AEA88736	Aea88736 Human ery	c 631	11.2	58.9	20	12	ADQ31326	Human XT-
c 559	11.4	60.0	29	15	AEF69792	Aef69792 Human L-P	c 632	11.2	58.9	20	13	ADQ31326	Human XT-
c 560	11.4	60.0	29	15	AEF69791	Aef69791 Human L-P	c 633	11.2	58.9	20	14	ADW38591	Hot flash
c 561	11.4	60.0	30	5	AAF84064	Aaf84064 5' and 3'	c 634	11.2	58.9	20	14	ADY60155	Antisense
c 562	11.4	60.0	30	10	ADH34370	Adh34370 Human t-P	c 635	11.2	58.9	20	14	ADZ84800	Murine so
c 563	11.4	60.0	30	14	ADZ36927	Adz36927 Rice ZnCe	c 636	11.2	58.9	21	2	AAV67434	Nucleotid
c 564	11.4	60.0	30	15	AEF00111	Aef00111 DNA probe	637	11.2	58.9	21	2	AAV67434	Nucleotid
c 565	11.2	58.9	15	8	ABZ69100	Abz69100 Fragment	638	11.2	58.9	21	2	AAZ26088	Human pol
c 566	11.2	58.9	15	10	ADF29171	Adf29171 Beta-glob	c 639	11.2	58.9	21	2	AAZ26088	Human pol
c 567	11.2	58.9	16	3	AAA48865	Aaa48865 Reverse p	640	11.2	58.9	21	4	AAAF95481	Human gen
c 568	11.2	58.9	17	8	ABT35415	Abt35415 Tumour su	641	11.2	58.9	21	4	AAH00829	Trypanoso
c 569	11.2	58.9	17	8	ACA06653	Aca06653 NFkB sub-	c 642	11.2	58.9	21	6	ABS98383	Human mul
c 570	11.2	58.9	17	8	ABZ61913	Abz61913 Human H-R	c 643	11.2	58.9	21	6	ABN85352	ds-protei
c 571	11.2	58.9	17	8	ABZ62012	Abz62012 Human H-R	c 644	11.2	58.9	21	10	ABZ80350	Human Emx
c 572	11.2	58.9	17	8	ACC65130	Acc65130 Murine ol	c 645	11.2	58.9	21	12	ADQ25174	MCAM mRNA
c 573	11.2	58.9	17	10	ADF62816	Adf62816 Human PCC	c 646	11.2	58.9	21	12	ADQ25174	MCAM mRNA
c 574	11.2	58.9	17	10	ADF62818	Adf62818 Human PCC	c 647	11.2	58.9	21	13	AEA97450	Human lup
c 575	11.2	58.9	17	11	ADL50606	Adl50606 Human PCR	648	11.2	58.9	21	14	ADV65744	Sense str
c 576	11.2	58.9	17	14	ADY67792	Ady67792 Autism ge	649	11.2	58.9	21	14	ADX45158	DNA probe
c 577	11.2	58.9	17	14	ADZ30987	Adz30987 Human H-R	650	11.2	58.9	21	14	ADX45158	DNA probe
c 578	11.2	58.9	17	14	ADZ31086	Adz31086 Human H-R	651	11.2	58.9	22	2	AAQ68315	Loc1-spec
c 579	11.2	58.9	18	8	ABZ76727	Abz76727 Cytolaem	652	11.2	58.9	22	2	AAV42511	PCR prime
c 580	11.2	58.9	18	10	ADG89466	Adg89466 Human mat	653	11.2	58.9	22	2	AAV42495	PCR prime
c 581	11.2	58.9	18	11	ADL61707	Adl61707 Human p16	654	11.2	58.9	22	2	AAV42495	PCR prime
c 582	11.2	58.9	18	11	ADM92691	Adm92691 SNP-conta	c 655	11.2	58.9	22	3	AAZ229172	Primer 10
c 583	11.2	58.9	18	14	AEC51557	Aec51557 Antisense	c 656	11.2	58.9	22	3	AAZ229172	Primer 10
c 584	11.2	58.9	18	14	AEC53955	Aec53955 Antisense	c 657	11.2	58.9	22	3	AAZ229172	Primer 10
c 585	11.2	58.9	18	14	AEC51584	Aec51584 Antisense	c 658	11.2	58.9	22	13	ADR03452	PCR prime
c 586	11.2	58.9	18	14	AEF31359	Aef31359 Cotton AR	c 659	11.2	58.9	22	14	ADV45283	Human Cpg
c 587	11.2	58.9	19	2	AAV47454	Aav47454 Feedback	c 660	11.2	58.9	22	14	ADV46033	Human Cpg
c 588	11.2	58.9	19	2	AAV93945	Aav93945 Primer RS	661	11.2	58.9	23	3	AAV30148	PCR prime
c 589	11.2	58.9	19	10	ADF54291	Adf54291 Human GAB	662	11.2	58.9	23	4	AAI65547	Primer fo
c 590	11.2	58.9	19	10	ADF53955	Adf53955 Human GAB	663	11.2	58.9	23	4	AAI65547	Primer fo
c 591	11.2	58.9	19	10	ADG34896	Adg34896 Human TNF	664	11.2	58.9	23	6	AAQ42937	Human PLA
c 592	11.2	58.9	19	10	ADG35019	Adg35019 Human TNF	665	11.2	58.9	23	12	ADJ62187	Human 143
c 593	11.2	58.9	19	14	ADZ85485	Adz85485 Methylati	666	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 594	11.2	58.9	19	14	AEC33540	Aec33540 Human GAB	c 667	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 595	11.2	58.9	19	14	AEC33204	Aec33204 Human GAB	c 668	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 596	11.2	58.9	19	14	AED44145	Aed44145 Human TNF	669	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 597	11.2	58.9	19	14	AED44145	Aed44145 Human TNF	670	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 598	11.2	58.9	19	14	AE55222	Aee55222 Human hai	c 671	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 599	11.2	58.9	19	14	AE55220	Aee55220 Human hai	c 672	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 600	11.2	58.9	19	14	AE55221	Aee55221 Human hai	c 673	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 601	11.2	58.9	19	14	AE55218	Aee55218 Human hai	674	11.2	58.9	24	2	AAQ28855	Probe Ol-
c 602	11.2	58.9	19	14	AE55225	Aee55225 Human hai	675	11.2	58.9	24	2	AAQ28855	Probe Ol-

676	11.2	58.9	24	3	AAC68613	Aac68613 Human G-C	749	11	57.9	11	6	AAL47358	Aa147358 Human NMD
c 677	11.2	58.9	24	3	AAC60811	Aac60811 Human BRC	750	11	57.9	11	8	ABx77662	Abx77662 Human N-m
c 678	11.2	58.9	24	4	AAS07427	Aas07427 PCR prime	751	11	57.9	11	9	ACD98327	Ac98327 Human NMD
c 679	11.2	58.9	24	4	ABL51702	Ab151702 Human GFR	752	11	57.9	11	10	AAD59659	Aad59659 Human NMD
c 680	11.2	58.9	24	6	AB572032	Ab572032 Human GFR	753	11	57.9	11	10	ABX98517	Abx98517 Human N-m
c 681	11.2	58.9	24	8	ABV75838	Abv75838 CD81 for	754	11	57.9	11	10	ABX92866	Abx92866 Human N-m
c 682	11.2	58.9	24	9	ADA45330	Ada45330 Human BRC	755	11	57.9	11	12	ADQ35259	Adq35259 Human hai
c 683	11.2	58.9	24	9	ADC07255	Ac07255 Human BRC	756	11	57.9	12	2	AAI14874	Aai14874 Triple he
c 684	11.2	58.9	24	10	ADC63308	Adc63308 Human BRC	757	11	57.9	13	5	AAX14866	Aax14866 Triple he
c 685	11.2	58.9	24	10	ADL01902	Adl01902 Human gra	758	11	57.9	13	5	ABC72338	Abc72338 Oligonuc
c 686	11.2	58.9	24	11	ADM13669	Adm13669 Oligonuc	759	11	57.9	13	5	ABF86424	Abf86424 Oligonuc
c 687	11.2	58.9	24	12	ADM86702	Adm86702 Human G-C	c 760	11	57.9	13	5	ABF86425	Abf86425 Oligonuc
c 688	11.2	58.9	24	12	ADMI2802	Admi2802 Single mu	c 761	11	57.9	13	5	ABC72339	Abc72339 Oligonuc
c 689	11.2	58.9	24	12	ADP98368	Adp98368 C. albica	c 762	11	57.9	15	4	AAI67334	Aai67334 Human FXB
c 690	11.2	58.9	25	2	AAQ76083	Aaq76083 HSV tk ge	c 763	11	57.9	17	3	AAF06237	Aaf06237 Hammerhea
c 691	11.2	58.9	25	4	AH78306	Aah78306 PCR prime	764	11	57.9	18	14	AEC25957	Aec25957 Human all
c 692	11.2	58.9	25	6	ABZ21959	Abz21959 Human Apo	765	11	57.9	18	14	AEC28323	Aec28323 Human all
c 693	11.2	58.9	25	6	ABL91161	Ab191161 Hominidae	766	11	57.9	19	2	AAQ38084	Aaq38084 PCR prime
c 694	11.2	58.9	25	6	ABR98501	Abra98501 TNFalpha	c 767	11	57.9	19	2	AAO5453	Aao5453 Primer 1
c 695	11.2	58.9	25	9	ACI66902	Aci66902 Human mic	c 768	11	57.9	19	2	AAQ03083	Aaq03083 p53 expre
c 696	11.2	58.9	25	9	ACI25049	Aci25049 Human mic	c 769	11	57.9	19	4	AAC90801	Aac90801 Human C-C
c 697	11.2	58.9	25	9	ACI73934	Aci73934 Human mic	770	11	57.9	19	14	AE42854	Aee42854 Human hai
c 698	11.2	58.9	25	10	ADF63559	Adf63559 Human PCC	c 771	11	57.9	19	14	AE42853	Aee42853 Human hai
c 699	11.2	58.9	25	10	ADF63569	Adf63569 Human PCC	c 772	11	57.9	19	15	AEF36779	Aef36779 Human SDF
c 700	11.2	58.9	25	14	ADZ28193	Adz28193 Neo gene	773	11	57.9	19	15	AEF36958	Aef36958 Human SDF
c 701	11.2	58.9	25	15	AE66295	Aee66295 Small int	c 774	11	57.9	20	3	AAA40890	Aaa40890 Murine TN
c 702	11.2	58.9	26	2	AX40765	Aax40765 Oligonuc	775	11	57.9	20	4	AAF23215	Aaf23215 Oligonuc
c 703	11.2	58.9	26	2	AX40797	Aax40797 Oligonuc	c 776	11	57.9	20	4	AAS08862	Aas08862 Human PD-
c 704	11.2	58.9	26	3	AAA10506	Aaa10506 PCR prime	c 777	11	57.9	20	4	AAS08771	Aas08771 Human PD-
c 705	11.2	58.9	26	4	AD13137	Ad13137 Human MTS	c 778	11	57.9	20	6	ABA83463	Ab83463 Human MP-
c 706	11.2	58.9	26	5	AAF62520	Aaf62520 Primer #1	c 779	11	57.9	20	6	ABA83462	Ab83462 Human MP-
c 707	11.2	58.9	26	6	ABK66444	Abk66444 Human gen	c 780	11	57.9	20	6	AAD46510	Aad46510 Human glu
c 708	11.2	58.9	26	10	ADC10394	Adc10394 Human NOV	c 781	11	57.9	20	9	ACD05118	Ac05118 Tumour ne
c 709	11.2	58.9	26	13	ADZ15701	Adz15701 Mutagenic	782	11	57.9	20	10	ADD20688	Add20688 Oreochrom
c 710	11.2	58.9	26	13	ADZ15702	Adz15702 Mutagenic	c 783	11	57.9	20	10	ADD69530	Add69530 Food enri
c 711	11.2	58.9	26	14	ABE98375	Ab98375 Rat GFAP	c 784	11	57.9	20	10	ADH76945	Adh76945 Lac Z A P
c 712	11.2	58.9	26	14	ABE90638	Ab90638 Rat GFAP	785	11	57.9	20	10	ABZ98854	Abz98854 Human PDE
c 713	11.2	58.9	26	14	ABE98412	Ab98412 Rat GFAP	786	11	57.9	20	10	ABZ93512	Abz93512 Human oli
c 714	11.2	58.9	26	14	ABE94256	Ab94256 Rat GFAP	787	11	57.9	20	11	ADM64961	Adm64961 NRY polym
c 715	11.2	58.9	26	14	ABE98678	Ab98678 Rat GFAP	788	11	57.9	20	11	ABD31885	Abd31885 Human PDE
c 716	11.2	58.9	26	14	ABE79133	Ab79133 Rat GFAP	789	11	57.9	20	11	ABD29742	Abd29742 A626698-
c 717	11.2	58.9	27	2	AAT35053	Aat35053 HSV thymi	c 790	11	57.9	20	12	ADQ60737	Adq60737 Oligonuc
c 718	11.2	58.9	27	2	AAZ233809	Aaz233809 Mouse Kv6	791	11	57.9	20	12	ADO46226	Ado46226 Human oli
c 719	11.2	58.9	27	2	AAZ83866	Aaz83866 Human lig	792	11	57.9	20	12	ADQ47461	Adq47461 S parvulu
c 720	11.2	58.9	27	4	ABH43365	Abh43365 KC (sense)	c 793	11	57.9	20	12	ADO29200	Ado29200 Mouse TNF
c 721	11.2	58.9	27	4	ABF84825	Aaf84825 PCR prime	c 794	11	57.9	20	13	ADR02716	Adr02716 Antisense
c 722	11.2	58.9	27	5	AAF27956	Aaf27956 Murine du	c 795	11	57.9	20	13	ADT00902	Adt00902 Novel mut
c 723	11.2	58.9	27	5	AAD02728	Aad02728 Human ABC	c 796	11	57.9	20	13	ADV97452	Adv97452 Hepatitis
c 724	11.2	58.9	27	6	ABK14711	Abk14711 PCR prime	c 797	11	57.9	20	14	ADY59632	Ady59632 C. utilis
c 725	11.2	58.9	27	14	AEA35032	Aea35032 Hb9 enhan	c 798	11	57.9	20	14	ADY60153	Ady60153 Antisense
c 726	11.2	58.9	28	4	AD02151	Ad02151 P. funicu	c 799	11	57.9	20	14	ABE95081	Aeb95081 Mouse eIF
c 727	11.2	58.9	28	6	AD035051	Ad035051 C. glutan	c 800	11	57.9	20	14	ABE94890	Aeb94890 Mouse eIF
c 728	11.2	58.9	28	9	ACC85468	Acc85468 T thermoh	c 801	11	57.9	20	14	AEC27442	Aec27442 Human all
c 729	11.2	58.9	28	13	ADW75898	Adw75898 Novel tra	c 802	11	57.9	21	2	AAX28531	Aax28531 Oligonuc
c 730	11.2	58.9	28	14	ADZ05923	Adz05923 Probe use	c 803	11	57.9	21	2	AAT07261	Aat07261 Primer fo
c 731	11.2	58.9	28	14	ABE02885	Aeb02885 Gene chip	c 804	11	57.9	21	2	AAT65566	Aat65566 Oligonuc
c 732	11.2	58.9	29	6	ABK49839	Abk49839 Mychis ta	c 805	11	57.9	21	2	AAX37123	Aax37123 Initiatin
c 733	11.2	58.9	29	8	ADA72303	Ada72303 Rice gene	c 806	11	57.9	21	2	AAX26726	Aax26726 PCR prime
c 734	11.2	58.9	29	14	ADX45157	Adx45157 DNA probe	c 807	11	57.9	21	4	AAI70247	Aai70247 Interleuk
c 735	11.2	58.9	30	2	AAQ93302	Aaq93302 Two membe	c 808	11	57.9	21	5	AAF22046	Aaf22046 Reverse P
c 736	11.2	58.9	30	2	AAT10602	Aat10602 CSF clone	c 809	11	57.9	21	5	AAH76327	Aah76327 Human FGF
c 737	11.2	58.9	30	2	ADP66310	Adp66310 Oligonuc	c 810	11	57.9	21	6	ABX00060	Abx00060 Human int
c 738	11.2	58.9	30	4	AAF70683	Aaf70683 2'NH2 RNA	c 811	11	57.9	21	9	ACC83441	Acc83441 PROC hypo
c 739	11.2	58.9	30	10	ADF43460	Adf43460 PCR prime	c 812	11	57.9	21	10	ADH16986	Adh16986 Human mtD
c 740	11.2	58.9	30	12	ADI28878	Adi28878 Human ser	c 813	11	57.9	21	10	ADU13100	Adj13100 Human DNA
c 741	11.2	58.9	30	12	ADO56474	Ado56474 Human cyc	c 814	11	57.9	21	12	ADU14315	Adj14315 DNA relat
c 742	11.2	58.9	30	12	ADP46371	Adp46371 PCR prime	c 815	11	57.9	21	13	ADQ92427	Adq92427 5-alpha r
c 743	11.2	58.9	30	14	ADM42937	Adm42937 Forward p	c 816	11	57.9	21	13	ADQ93717	Adq93717 3-beta-hy
c 744	11.2	58.9	30	15	AEF07299	Aef07299 SPUIVE SNP	c 817	11	57.9	21	13	ADQ93536	Adq93536 3-beta-hy
c 745	11	57.9	11	2	AAQ79374	Aaq79374 Human NMD	c 818	11	57.9	21	13	ADR18381	Adr18381 Human GOB
c 746	11	57.9	11	2	AAV82891	Aav82891 Inbert pr	c 819	11	57.9	21	13	ADR18469	Adr18469 Human GOB
c 747	11	57.9	11	3	AAZ38705	Aaz38705 Human NMD	c 820	11	57.9	21	14	ADW72549	Adw72549 Mitochond
c 748	11	57.9	11	6	ABI99171	Abi99171 Human NMD	c 821	11	57.9	21	14	ADW72547	Adw72547 Mitochond

822	11	57.9	21	14	ADW72548	Adw72548 Mitochond	895	11	57.9	27	6	ABK53065	Abk53065 S. Cerevi
c 823	11	57.9	21	14	AEC65320	Aec65320 DNA for s	896	11	57.9	27	7	ADI93703	Adi93703 Murine IL
c 824	11	57.9	21	14	AEb99780	AEb99780 DNA encod	897	11	57.9	27	7	ADI94659	Adi94659 FRET olig
825	11	57.9	21	15	AEE28389	Aee28389 Escherich	c 898	11	57.9	27	8	ABV72381	Abv72381 PCR prime
826	11	57.9	21	15	AEF02561	Aef02561 Escherich	c 899	11	57.9	27	10	ADG38359	Adg38359 Anti-HIV
c 827	11	57.9	22	2	AAQ95239	AAq95239 Simple ta	900	11	57.9	27	10	ABZ95568	Abz95568 Human end
828	11	57.9	22	2	AAQ95239	AAq95239 Simple ta	901	11	57.9	27	11	ABD19718	Abd19718 Human end
829	11	57.9	22	4	AAQ24806	AAq24806 PCR prime	902	11	57.9	27	13	ADT77699	Adt77699 Neisseria
c 830	11	57.9	22	4	AAQ24806	AAq24806 PCR prime	903	11	57.9	27	13	ADY27216	Ady27216 Human CX
c 831	11	57.9	22	4	AAF32208	AAf32208 Arabidops	c 904	11	57.9	27	13	ADZ47977	Adz47977 DESCL rel
c 832	11	57.9	22	10	ADD19577	Ad19577 Oreochrom	c 905	11	57.9	27	13	ADZ47977	Adz47977 DESCL rel
c 833	11	57.9	22	11	ADZ09135	Adz09135 Novel DNA	c 906	11	57.9	27	14	AEC07377	Aec07377 Herpes vi
c 834	11	57.9	22	12	ADI28447	Adi28447 Arabidops	c 907	11	57.9	27	14	AEC07384	Aec07384 Herpes vi
c 835	11	57.9	23	2	AAQ59051	AAq59051 Human tra	c 908	11	57.9	28	2	AAQ22980	AAq22980 Canine BP
c 836	11	57.9	23	3	AAQ66148	AAq66148 21-hydrox	c 909	11	57.9	28	5	AAF58388	AAf58388 Murine GM
c 837	11	57.9	23	3	AAQ66152	AAq66152 21-hydrox	910	11	57.9	28	10	ADF39553	Adf39553 SFRP5 gen
c 838	11	57.9	23	14	ADV45600	Adv45600 Human CpG	911	11	57.9	28	12	ADN36198	Adn36198 Probe #27
839	11	57.9	23	15	AEP21532	Aef21532 Human non	912	11	57.9	28	12	ADN36201	Adn36201 Probe #28
c 840	11	57.9	24	6	AAQ16482	AAq16482 Rat (Na,K	913	11	57.9	28	12	ADN36193	Adn36193 Probe #27
c 841	11	57.9	24	10	ADD35579	Ad35579 Escherich	914	11	57.9	28	12	ADN36195	Adn36195 Probe #27
c 842	11	57.9	24	10	ACH00666	Ach00666 Mammalian	915	11	57.9	28	12	ADN36194	Adn36194 Probe #27
c 843	11	57.9	24	10	ADF79194	Adf79194 PSA PCR p	916	11	57.9	28	12	ADN36200	Adn36200 Probe #28
c 844	11	57.9	24	13	ADT62653	Adt62653 Genetic p	917	11	57.9	28	12	ADN36199	Adn36199 Probe #28
c 845	11	57.9	24	13	ADV34197	Adv34197 Improved	918	11	57.9	28	12	ADN36202	Adn36202 Probe #28
c 846	11	57.9	24	14	ADZ44637	Adz44637 PCR prime	919	11	57.9	28	12	ADN36196	Adn36196 Probe #27
c 847	11	57.9	25	2	AAQ20094	AAq20094 Cytomegal	920	11	57.9	28	12	ADN36197	Adn36197 Probe #27
c 848	11	57.9	25	2	AAQ58565	AAq58565 CMV MIE g	921	11	57.9	29	3	AAA04353	AAA04353 Polymorph
c 849	11	57.9	25	2	AAQ28532	AAq28532 Oligonuc	922	11	57.9	29	3	AAQ4167	AAq4167 Polymorph
c 850	11	57.9	25	2	AAQ76059	AAq76059 hCMV Prim	923	11	57.9	29	3	AAQ34541	AAq34541 DNA seque
c 851	11	57.9	25	2	AAQ65567	AAq65567 Oligonuc	c 924	11	57.9	29	3	AAQ34542	AAq34542 DNA seque
c 852	11	57.9	25	2	AAV07715	AAv07715 Cytomegal	c 925	11	57.9	29	5	AAH45090	AAh45090 Murine in
c 853	11	57.9	25	2	AAQ91197	AAq91197 CMV imm	c 926	11	57.9	29	10	ADA01460	Ada01460 Mouse ang
c 854	11	57.9	25	3	AAQ82992	AAq82992 CMV detec	c 927	11	57.9	29	12	ADN94975	Adn94975 Rat fatty
c 855	11	57.9	25	3	AAQ59161	AAq59161 Primer #2	c 928	11	57.9	29	14	ADX70075	Adx70075 Mouse p16
c 856	11	57.9	25	4	AAH21680	AAh21680 Human cyt	c 929	11	57.9	30	2	AAQ230102	AAq230102 PCR prime
c 857	11	57.9	25	4	AAH21688	AAh21688 Human cyt	c 930	11	57.9	30	2	AAQ28083	AAq28083 Murine IL
c 858	11	57.9	25	4	AAH21688	AAh21688 Human cyt	c 931	11	57.9	30	2	AAQ28083	AAq28083 Murine IL
c 859	11	57.9	25	6	ABX00061	ABx00061 Human int	c 932	11	57.9	30	5	AAQ595132	AAq595132 Otofelin
c 860	11	57.9	25	6	ABX00061	ABx00061 Human int	c 933	11	57.9	30	5	AAQ595132	AAq595132 Otofelin
861	11	57.9	25	6	ABK70483	ABk70483 In-situ a	c 934	11	57.9	30	6	ABA99121	AbA99121 Sense pri
c 862	11	57.9	25	9	ACI28450	ACi28450 Human mic	935	11	57.9	30	6	AAQ149448	AAq149448 High thro
c 863	11	57.9	25	9	ACI60867	ACi60867 Human mic	936	11	57.9	30	7	ADI93711	Adi93711 Murine IL
c 864	11	57.9	25	9	ACI60867	ACi60867 Human mic	c 937	11	57.9	30	7	ADI93717	Adi93717 Murine IL
c 865	11	57.9	25	9	ACI73108	ACi73108 Human mic	c 938	11	57.9	30	7	ADI93872	Adi93872 Human IL
c 866	11	57.9	25	9	ACI41114	ACi41114 Human mic	c 939	11	57.9	30	10	ADD42609	Ad42609 Human inf
c 867	11	57.9	25	9	ACH51542	ACH51542 DNA targe	c 940	11	57.9	30	12	ADP08610	Adp08610 PCR prime
c 868	11	57.9	25	9	ACH51543	ACH51543 DNA targe	c 941	11	57.9	30	12	ADP08610	Adp08610 PCR prime
c 869	11	57.9	25	11	ADL59803	ADl59803 Arabidops	c 942	11	57.9	30	14	AEI11717	Aei11717 Endonucle
c 870	11	57.9	25	12	ADJ14316	ADj14316 DNA relat	c 943	11	57.9	30	14	AEI11717	Aei11717 Endonucle
c 871	11	57.9	25	13	ADL15565	ADl15565 Mouse flo	c 944	11	57.9	30	15	AEF07567	Aef07567 PFTK1 SNP
c 872	11	57.9	25	14	ADY81843	ADy81843 Thale-cra	c 945	10.8	56.8	14	2	ADG14093	Adg14093 Porcine r
c 873	11	57.9	25	14	ADY81843	ADy81843 Thale-cra	c 946	10.8	56.8	15	4	AAQ04330	AAq04330 Human DAX
c 874	11	57.9	25	14	ADY81843	ADy81843 Thale-cra	c 947	10.8	56.8	15	10	ADF83518	Adf83518 Human MCL
c 875	11	57.9	25	14	ADY81843	ADy81843 Thale-cra	c 948	10.8	56.8	15	12	ADH70514	Adh70514 Human Vbe
c 876	11	57.9	25	15	ADY81843	ADy81843 Thale-cra	c 949	10.8	56.8	15	12	ADH70514	Adh70514 Human Vbe
c 877	11	57.9	26	2	AAQ04998	AAq04998 Sequence	c 950	10.8	56.8	16	5	AAQ15521	AAq15521 N-acetyl
c 878	11	57.9	26	2	AAQ33261	AAq33261 Triplex f	c 951	10.8	56.8	16	6	AAI68609	AAi68609 ICAM-1 tr
c 879	11	57.9	26	2	AAQ36286	AAq36286 EGFR2par	c 952	10.8	56.8	16	14	ADW01656	Adw01656 DNA oligo
c 880	11	57.9	26	2	AAQ36287	AAq36287 EGFR2anti	c 953	10.8	56.8	16	14	ADW01656	Adw01656 DNA oligo
c 881	11	57.9	26	2	AAQ40790	AAq40790 Oligonuc	c 954	10.8	56.8	17	2	AAAT81044	AAa81044 Human c-m
c 882	11	57.9	26	2	AAQ40756	AAq40756 Oligonuc	c 955	10.8	56.8	17	2	AAQ63959	AAq63959 Rabbit st
c 883	11	57.9	26	3	AAQ96685	AAq96685 PCR prime	c 956	10.8	56.8	17	3	AAQ70759	AAq70759 Hammerhea
c 884	11	57.9	26	3	AAQ96685	AAq96685 PCR prime	c 957	10.8	56.8	17	3	AAQ73558	AAq73558 Reverse p
c 885	11	57.9	26	3	AAQ96685	AAq96685 PCR prime	c 958	10.8	56.8	17	4	ABK00896	ABk00896 Human NOG
c 886	11	57.9	26	13	ADR32549	ADR32549 Human nic	c 959	10.8	56.8	17	4	ABK00897	ABk00897 Human NOG
c 887	11	57.9	26	13	ADR32549	ADR32549 Human nic	c 960	10.8	56.8	17	4	ABK00899	ABk00899 Human NOG
c 888	11	57.9	27	2	AAQ15632	AAq15632 Viral int	c 961	10.8	56.8	17	4	ABK00899	ABk00899 Human NOG
c 889	11	57.9	27	2	AAQ76517	AAq76517 Endotheli	c 962	10.8	56.8	17	5	ADV03317	Adv03317 Human BAC
c 890	11	57.9	27	2	AAQ79221	AAq79221 Oligonuc	c 963	10.8	56.8	17	5	ADV47057	Adv47057 HBV inozy
c 891	11	57.9	27	3	AAQ54308	AAq54308 Endotheli	c 964	10.8	56.8	17	5	ADV47056	Adv47056 HBV inozy
c 892	11	57.9	27	3	AAQ93171	AAq93171 Primer B	c 965	10.8	56.8	17	5	ADV47056	Adv47056 HBV inozy
c 893	11	57.9	27	3	AAQ33752	AAq33752 Low adeno	c 966	10.8	56.8	17	5	ADV47972	Adv47972 HBV G-cl
c 894	11	57.9	27	3	AAQ33752	AAq33752 Low adeno	c 967	10.8	56.8	17	5	ADV61258	Adv61258 HBV amber
c 895	11	57.9	27	5	AAQ04265	AAq04265 Saccharom							

c 968 10.8 56.8 17 5 ADV48340
 c 969 10.8 56.8 17 5 ADV49040 HBV DNAzy
 c 970 10.8 56.8 17 6 ABO02323 Human GDM
 c 971 10.8 56.8 17 6 ABO02322 Human GDM
 c 972 10.8 56.8 17 6 ABO02320 Human GDM
 c 973 10.8 56.8 17 6 ABO02321 Human GDM
 c 974 10.8 56.8 17 6 ABO06801 Human GDM
 c 975 10.8 56.8 17 6 ABO06797 Human GDM
 c 976 10.8 56.8 17 6 ABO98503 Human ace
 c 977 10.8 56.8 17 6 ACN11587 WNV minus
 c 978 10.8 56.8 17 6 ACN03787 WNV Zinzy
 c 979 10.8 56.8 17 6 ACN04889 WNV DNAzy
 c 980 10.8 56.8 17 6 ACN05903 WNV Amber
 c 981 10.8 56.8 17 6 ACN11588 WNV minus
 c 982 10.8 56.8 17 6 ABO36139 Tumour su
 c 983 10.8 56.8 17 8 ACA09149 NFKB sub-
 c 984 10.8 56.8 17 8 ACA09172 NFKB sub-
 c 985 10.8 56.8 17 8 ACA09148 NFKB sub-
 c 986 10.8 56.8 17 8 ABZ60669 Human K-R
 c 987 10.8 56.8 17 8 ABZ65426 Human HER
 c 988 10.8 56.8 17 8 ABZ65427 Human HER
 c 989 10.8 56.8 17 8 ACD53277 HBV G-cle
 c 990 10.8 56.8 17 8 ACD53278 HBV inozy
 c 991 10.8 56.8 17 8 ACD53277 HBV inozy
 c 992 10.8 56.8 17 8 ACC66572 Murine ol
 c 993 10.8 56.8 17 10 ADB41031 Tumour su
 c 994 10.8 56.8 17 12 ADM58921 Hepatitis
 c 995 10.8 56.8 17 12 ADM59380 Hepatitis
 c 996 10.8 56.8 17 12 ADM58922 Hepatitis
 c 997 10.8 56.8 17 13 ACN69891 Human GDM
 c 998 10.8 56.8 17 13 ACN69887 Human GDM
 c 999 10.8 56.8 17 13 ACN65410 Human GDM
 c1000 10.8 56.8 17 13 ACN65411 Human GDM

ALIGNMENTS

RESULT 1
 ADF17589 ID ADF17589 standard; DNA; 22 BP.
 XX
 AC ADF17589;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Beta A PCR primer SEQ ID NO:1.
 XX
 KW neovascularisation agent; activin stimulator;
 KW anti-neovascularisation agent; activin inhibitor;
 KW neovascularisation regulator; ischaemic condition; atherosclerosis;
 KW occlusive arteriosclerosis; lower limb vascular occlusion;
 KW myocardial infarction; angina pectoris; cerebral embolism;
 KW recalcitrant skin ulcer; diabetes; pancreatic islet cell regeneration;
 KW diabetic retinopathy; senile macular degeneration;
 KW chronic rheumatoid arthritis; cancer; psoriasis vulgaris; PCR primer;
 KW beta A; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003094966-A1.
 XX
 PD 20-NOV-2003.
 XX
 PF 12-MAY-2003; 2003WO-JP005901.
 XX
 PR 10-MAY-2002; 2002JP-00135575.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 XX
 PI Kojima I, Maeshima K, Eto Y;
 XX
 DR WPI; 2003-903943/82.

XX Agents promoting or suppressing neovascularization containing activin
 PT stimulator or activin inhibitor, to treat ischemic conditions, diabetes
 PT and skin ulcers, or rheumatoid arthritis, diabetic retinopathy and
 PT cancer, etc.
 XX
 PS Example 2; SEQ ID NO 1; 37pp; Japanese.
 XX
 CC The present invention describes a neovascularisation agent (I), which has
 CC an activin stimulator as an active component. Also described: (1) an anti
 CC -neovascularisation agent (II) containing an activin inhibitor as an
 CC active component; and (2) a neovascularisation regulator comprising (I)
 CC and (II). The neovascularisation agent (I) can be used to prevent or
 CC treat ischaemic conditions, atherosclerosis, occlusive arteriosclerosis,
 CC lower limb vascular occlusion, myocardial infarction, angina pectoris,
 CC cerebral embolism, recalcitrant skin ulcers; and diabetes, through
 CC pancreatic islet cell regeneration. The anti-neovascularisation agent
 CC (II) can be used to prevent or treat diabetic retinopathy, senile macular
 CC degeneration, chronic rheumatoid arthritis, cancer, psoriasis vulgaris.
 CC The present sequence represents a PCR primer for beta A, which is used in
 CC an example from the present invention.
 XX
 SQ Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;
 Query Match 77.9%; Score 14.8; DB 10; Length 22;
 Best Local Similarity 88.9%; Pred. No. 8.6e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GGAGAGGGGTGGTGC 18
 Db 5 GGAGAGGGGTGGTGC 22
 RESULT 2
 ABO10197
 ID ABO10197 standard; DNA; 26 BP.
 XX
 AC ABO10197;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE S. aggregatum Delta4-desaturase PCR primer RO1239.
 XX
 KW ss; PCR; primer; delta4-desaturase; polyunsaturated fatty acid; PUFA;
 KW nutritional; cosmetic; pharmaceutical; animal feed;
 KW omega6-docosaenoic acid; docosahexaenoic acid; restenosis;
 KW angioplasty; inflammation; rheumatoid arthritis; asthma; psoriasis;
 KW osteoporosis; kidney stone; urinary tract stone; cancer; cachexia;
 KW cancer; diabetes; eczema; gastrointestinal bleeding; endometriosis;
 KW premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue;
 KW viral infections; acquired immunodeficiency syndrome; AIDS;
 KW multiple sclerosis; inflammatory skin disorder; blood pressure;
 KW platelet aggregation; vasodilation; cholesterol level.
 XX
 OS Schizochytrium aggregatum.
 XX
 PN WO200290493-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 02-MAY-2002; 2002WO-US013589.
 XX
 PR 04-MAY-2001; 2001US-00849199.
 PR 11-APR-2002; 2002US-00120637.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Huang Y, Das T, Thurmond JM, Leonard AB, Pereira SL;
 XX
 DR WPI; 2003-058927/05.
 XX
 PT Novel purified Delta4-desaturase enzymes which desaturates
 PT polyunsaturated fatty acids at carbon 4, useful for producing

PT polynsaturated fatty acids which are used for treating diabetes, kidney
PT stones, endometriosis.
PS Example 7; Page 55; 174pp; English.
XX
XX The invention relates to a purified polypeptide, Delta4-desaturase which
CC desaturates polyunsaturated fatty acids (PUFA) at carbon 4, isolated from
CC Schizochytrium aggregatum or Thraustochytrium aureum. Also included are
CC nucleotide sequences encoding the desaturases (including sequences 50%
CC similar to them), a vector comprising the nucleotide sequence, a host
CC cell comprising the vector, a transgenic plant cell or tissue comprising
CC the vector and thereby producing PUFA via expression of the desaturase
CC and a composition comprising at least omega6-docosapentaenoic acid and
CC docosahexaenoic acid, produced using the desaturase. The desaturase
CC protein and nucleotide are useful for producing the final product PUFA
CC omega6-docosapentaenoic acid or docosahexaenoic acid from the substrate
CC PUFAs linoleic acid, gamma-linolenic acid, stearidonic acid, arachidonic
CC acid, dihomo-gamma-linolenic acid, eicosatetraenoic acid, adrenic acid,
CC or eicosapentaenoic acid. The final product PUFA is omega6-
CC docosapentaenoic acid and docosahexaenoic acid. The composition is useful
CC for treating or preventing a condition caused by insufficient intake of
CC PUFA (e.g. restenosis after angioplasty, inflammation, rheumatoid
CC arthritis, asthma, psoriasis, osteoporosis, kidney or urinary tract
CC stones, cancer, cachexia associated with cancer, diabetes, eczema,
CC gastrointestinal bleeding, endometriosis and premenstrual syndrome,
CC myalgic encephalomyelitis, chronic fatigue after viral infections,
CC acquired immunodeficiency syndrome (AIDS), multiple sclerosis and
CC inflammatory skin disorders). The omega6-Docosapentaenoic acid and
CC docosahexaenoic acid produced may be added to nutritional compositions
CC (e.g. infant supplements), pharmaceutical compositions, cosmetics and
CC animal feeds. The composition is also useful for e.g. reducing blood
CC pressure, inhibiting platelet aggregation, inducing vasodilation,
CC reducing cholesterol levels. The present sequence is a PCR primer used to
CC isolate nucleic acids encoding the delta4-desaturase enzymes of the
XX invention
XX
SQ Sequence 26 BP; 6 A; 4 C; 12 G; 4 T; 0 U; 0 Other;
Query Match 74.7%; Score 14.2; DB 8; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CGAGAGGGGGTGGGTGCT 19
DB 2 CGAGCATGGGTAGGTGCT 20
RESULT 3
ABZ70091
ID ABZ70091 standard; DNA; 30 BP.
XX
XX ABZ70091;
XX
XX 10-APR-2003 (first entry)
XX
XX Human chromosome 22-related PCR primer, 553-F5, SEQ ID 7.
DE
XX PCR; primer; human artificial chromosome; antibody lambda light chain;
KW chromosome 22; human; transgenic; antibody drug; infection; ss.
XX
XX Homo sapiens.
OS
XX WO200292812-A1.
XX
XX 21-NOV-2002.
XX
XX 10-MAY-2002; 2002WO-JP004587.
XX
XX 11-MAY-2001; 2001JP-00142371.
XX
XX (KIRI) KIRIN BEER KK.
PA (MEDA-) MEDAREX INC.
XX

PI Kuroiwa Y, Tomizuka K, Yoshida H, Ishida I;
XX
XX WPI; 2003-129293/12.
XX
XX Artificial human chromosome containing human antibody lambda light chain
PT gene transferred to offspring via non-human genital system for
PT constructing transchromosomal mice, applicable in developing human
PT antibody drugs.
XX
XX Example 5; Page 22; 64pp; Japanese.
XX
XX The present invention relates to a human artificial chromosome, which can
CC be transferred to offspring via a non-human genital system. The human
CC artificial chromosome carries the antibody lambda light chain gene
CC (originally from the human chromosome 22) ligated to another chromosome
CC fragment from another human chromosome. The human artificial chromosome
CC can be used to generate transgenic mice, which are useful for producing
CC human antibodies and in developing human antibody drugs for treatment of
CC e.g. infections. The present sequence is a PCR primer, which was used in
CC an example from the invention
XX
SQ Sequence 30 BP; 12 A; 3 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 74.7%; Score 14.2; DB 8; Length 30;
Best Local Similarity 84.2%; Pred. No. 1.5e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAGAGGGGGTGGGTGCT 19
DB 2 GAAGAGAGGAGTGGGTGCT 20
RESULT 4
AAT86507/c
ID AAT86507 standard; DNA; 20 BP.
XX
XX AAT86507;
XX
XX 12-MAR-1998 (first entry)
XX
XX S-adenosylmethionine decarboxylase antisense oligonucleotide #8.
DE
XX
KW S-adenosylmethionine decarboxylase; SAMDC; antisense oligonucleotide;
KW antitumour; diagnosis; phosphorothioate; psoriasis; spermine; spermidine;
KW ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /note= "nucleotides are bonded via phosphorothioate
FT linkages"
XX
XX WO9605298-A1.
XX
XX 22-FEB-1996.
XX
XX 27-JUL-1995; 95WO-EP002985.
XX
XX 09-AUG-1994; 94US-00287753.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX Mett H, Haner R, Dean NM;
XX
XX WPI; 1996-139694/14.
XX
XX New oligo:nucleotide derive. specific for S-adenosyl:methionine
PT decarboxylase related nucleic acid - useful as anti:sense inhibitors of
PT this enzyme, esp. for treatment of tumours but also as hybridisation
PT probes for diagnosis.
PT

XX Example 8; Page 45; 81pp; English.

PS This sequence represents a phosphorothioate analogue of an antisense

CC oligonucleotide which targets the 3' untranslated region of S-

CC adenosylmethionine decarboxylase (SAMDC) around nucleotides at positions

CC 1046 to 1065. Antisense oligonucleotide analogues (AAT86500-14) which

CC target the SAMDC gene are used to diagnose conditions associated with

CC expression of SAMDC by specifically hybridising to RNA or DNA derived

CC from the SAMDC gene. These antisense molecules are useful for therapeutic

CC modulation (especially inhibition) of SAMDC synthesis, particularly to

CC treat tumours (e.g. leukaemia, prostatic carcinoma, colon or brain

CC tumours, but especially bladder cancer), but also other hyper-

CC proliferative diseases such as psoriasis. They cause tumour regression

CC and prevent establishment/growth of (micro)metastases. Inhibition of

CC SAMDC reduces the level of polyamines (spermine and spermidine in cells),

CC resulting in cytostasis and possibly apoptosis

XX Sequence 20 BP; 7 A; 8 C; 1 G; 4 T; 0 U; 0 Other;

SQ Query Match 72.6%; Score 13.8; DB 2; Length 20;

Best Local Similarity 88.2%; Pred. No. 2.2e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGTGCT 19

DB 19 AGAAGGGTGGTGATGCT 3

RESULT 5

ADK23254

ID ADK23254 standard; DNA; 20 BP.

XX AC ADK23254;

XX DT 18-NOV-2004 (first entry)

XX DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3331.

XX acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;

KW metabolic syndrome X; cardiovascular disorder; cancer; infection;

KW inflammation; tumour; antisense; ss.

XX OS Synthetic.

XX WO2004016749-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025389.

XX PR 14-AUG-2002; 2002US-0403591P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Ross SA;

XX WPI; 2004-203782/19.

XX New antisense compounds targeted to nucleic acid molecules encoding acyl-

PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or

PT conditions associated with aberrant expression of ACS1, e.g. diabetes,

PT obesity or cancer.

XX Claim 3; SEQ ID NO 3331; 940pp; English.

XX The invention relates to an antisense compound targeted to a nucleic acid

CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense

CC compound specifically hybridises with and inhibits the expression of

CC ACS1. The antisense oligonucleotides or compounds are useful for

CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for

PT treating diseases or conditions associated with aberrant expression of

PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or

PT conditions associated with aberrant expression of ACS1, e.g. diabetes,

PT obesity or cancer.

XX Claim 3; SEQ ID NO 3331; 940pp; English.

XX The invention relates to an antisense compound targeted to a nucleic acid

CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense

CC compound specifically hybridises with and inhibits the expression of

CC ACS1. The antisense oligonucleotides or compounds are useful for

CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for

CC treating diseases or conditions associated with aberrant expression of

CC ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular

CC disorder or cancer. The antisense compounds are also useful as research

CC reagents and kits, or in diagnostic, therapeutic and prophylactic

CC applications, e.g. to prevent or delay infection, inflammation or tumour

CC formation. The present sequence represents an acyl-coenzyme A synthetase

CC 1, ACS1, antisense oligonucleotide.

XX Sequence 20 BP; 4 A; 3 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 13; Length 20;

Best Local Similarity 88.2%; Pred. No. 2.2e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGTGCT 19

DB 3 AGAAGGTGGTGATGCT 19

RESULT 6

ADK23371

ID ADK23371 standard; DNA; 20 BP.

XX AC ADK23371;

XX DT 18-NOV-2004 (first entry)

XX DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3448.

XX acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;

KW metabolic syndrome X; cardiovascular disorder; cancer; infection;

KW inflammation; tumour; antisense; ss.

XX OS Synthetic.

XX WO2004016749-A2.

XX PD 26-FEB-2004.

XX PF 14-AUG-2003; 2003WO-US025389.

XX PR 14-AUG-2002; 2002US-0403591P.

XX PA (PHAA) PHARMACIA CORP.

XX PI Ross SA;

XX WPI; 2004-203782/19.

XX New antisense compounds targeted to nucleic acid molecules encoding acyl-

PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or

PT conditions associated with aberrant expression of ACS1, e.g. diabetes,

PT obesity or cancer.

XX Claim 3; SEQ ID NO 3448; 940pp; English.

XX The invention relates to an antisense compound targeted to a nucleic acid

CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense

CC compound specifically hybridises with and inhibits the expression of

CC ACS1. The antisense oligonucleotides or compounds are useful for

CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for

CC treating diseases or conditions associated with aberrant expression of

CC ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular

CC disorder or cancer. The antisense compounds are also useful as research

CC reagents and kits, or in diagnostic, therapeutic and prophylactic

CC applications, e.g. to prevent or delay infection, inflammation or tumour

CC formation. The present sequence represents an acyl-coenzyme A synthetase

CC 1, ACS1, antisense oligonucleotide.

XX Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 13; Length 20;

Best Local Similarity 88.2%; Pred. No. 2.2e+04;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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PD 19-JAN-2006.
XX
XX
PF 28-JUN-2005; 2005WO-JP011810.
XX
XX
PR 08-JUL-2004; 2004JP-00201895.
XX
XX (NIHE-) JAPAN HEALTH SCI FOUND.
XX
XX Takahashi M, Kamei Y, Ezaki O;
XX
XX WPI; 2006-110104/11.
XX
XX Diagnosing obesity-related diseases by measuring expression of mesoblast-
XX specific transcript (Mest) in adipocytes, useful in clinical examination
XX and in screening drugs in the treatment of, e.g. diabetes.
XX
XX Disclosure; SEQ ID NO 2; 34pp; Japanese.
XX
XX The invention relates to a method of diagnosing obesity-related diseases
XX comprising measuring the expression doses of mesoblast-specific
XX transcript (Mest) in adipocytes. The invention also relates to a method
XX of examining whether or not a test substance is a Mest expression
XX controller comprising the administration of the test substance to an
XX animal for laboratory use, measuring the amount of Mest mRNA in
XX adipocytes of the animal or the amount of Mest protein in its blood and
XX determining whether or not the test substance can cause a change in the
XX Mest mRNA expression dose, and a method of screening a Mest expression
XX controller. To assay the Mest expression dose, the amount of Mest mRNA in
XX adipocytes or the amount of Mest protein in blood is measured. The method
XX is useful in clinical examination and in screening of expression
XX controllers as drugs in the treatment or management of, e.g. obesity,
XX type II diabetes, arteriosclerosis, hypertension and hyperlipemia. This
XX sequence represents a PCR primer used to amplify Mest cDNA of the
XX invention.
XX
XX Sequence 20 BP; 5 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 15; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
Db 19 AGAAGTGGGTGAGTGT 3

RESULT 10
ADN00574/c
ID ADN00574 standard; DNA; 21 BP.
XX
XX ADN00574;
XX
XX 17-JUN-2004 (first entry)
XX
XX Murine adipocyte P2 (ap2) PCR primer #2.
XX
XX Osteoblastic differentiation induction; osteoblastic differentiation;
XX mesenchymal stem cell; oxysterol; adipocyte differentiation inhibition;
XX adipocyte differentiation; adipogenesis; adipogenic gene;
XX lipoprotein lipase; LPL; adipocyte P2; ap2; murine; PCR; primer; ss.
XX
XX Mus sp.
XX
XX WO2004019884-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027105.
XX
XX 29-AUG-2002; 2002US-0406715P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX

PI Parhami F;
XX
XX WPI; 2004-257333/24.
XX
XX Use of oxysterol to induce osteoblastic differentiation and bone
XX formation to increase bone mass and inhibit adipocyte differentiation in
XX mammalian mesenchymal stem cells.
XX
XX Disclosure; Page 15; 47pp; English.
XX
XX The present invention relates to a method for induction of osteoblastic
XX differentiation in mammalian mesenchymal stem cells. The method comprises
XX administration of at least one oxysterol (A). (A) is used to induce
XX osteoblastic differentiation and inhibit adipocyte differentiation in
XX mammalian mesenchymal stem cells and treat mammalian mesenchymal cells.
XX (A) is administered at a selected interval together with at least one
XX secondary agent (such as parathyroid hormone, sodium fluoride, insulin-
XX like growth factor I, insulin-like growth factor II or transforming
XX growth factor beta) to increase the differentiation of marrow stromal
XX cells into osteoblasts and to increase the number of osteoblasts present
XX in bone tissue, induce bone formation to increase bone mass and treat
XX osteoporosis to ameliorate the symptoms of osteoporosis. In an example
XX from the invention, adipogenesis was assessed by an inhibition of
XX expression of adipogenic genes lipoprotein lipase (LPL) and adipocyte P2
XX (ap2) by (A) using PCR primers ADN00573-ADN00576.
XX
XX Sequence 21 BP; 4 A; 10 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 12; Length 21;
Best Local Similarity 88.2%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGCT 19
Db 18 AGAAGTGGGTGAGTGT 2

RESULT 11
ADY38715/c
ID ADY38715 standard; DNA; 21 BP.
XX
XX ADY38715;
XX
XX 19-MAY-2005 (first entry)
XX
XX Mouse adipocyte protein 2 (ap2) PCR primer #2.
XX
XX differentiation; stem cell; osteopathic; bone repair; bone degeneration;
XX osteoporosis; ap2; adipocyte protein 2; PCR; primer; ss.
XX
XX Mus musculus.
XX
XX WO2005020928-A2.
XX
XX 10-MAR-2005.
XX
XX 30-AUG-2004; 2004WO-US028162.
XX
XX 29-AUG-2003; 2003US-0499040P.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Parhami F;
XX
XX WPI; 2005-214410/22.
XX
XX Induction of osteoblastic differentiation of mammalian mesenchymal stem
XX cells includes treating mammalian mesenchymal cells with at least one
XX oxysterol and at least one bone morphogenic protein.
XX
XX Example; Page 16; 52pp; English.
XX
XX This invention relates to a novel method of induction of osteoblastic

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CC differentiation of mammalian mesenchymal stem cells. The method includes
 CC treating mammalian mesenchymal cells with at least one oxysterol and at
 CC least one bone morphogenic protein (BMP). The invention may be useful for
 CC the development of compounds with an osteopathic activity acting as
 CC adipocyte differentiation of MSC inhibitors, osteoblastic differentiation
 CC of MSC inducers or Liver X receptors (LXR) activators. The invention may
 CC be useful to induce osteoblastic differentiation of mammalian mesenchymal
 CC stem cells (MSC), to stimulate mammalian cells to express a level of a
 CC biological marker of osteoblastic differentiation, to inhibit adipocyte
 CC differentiation of MSC, to increase the differentiation of marrow stromal
 CC cells into osteoblasts and to induce bone formation (endochondral or
 CC intramembraneous bone formation) and to treat/ameliorate a patient
 CC exhibiting clinical symptoms of osteoporosis. The method is very
 CC effective in treating bone disorders without side effects. The present
 CC sequence is that of a PCR primer which was used for amplification of a
 CC region of the mouse adipocyte protein 2 (ap2)-encoding gene in the
 CC exemplification of the invention.

XX Sequence 21 BP; 4 A; 10 C; 1 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 72.6%; Score 13.8; DB 14; Length 21;
 Best Local Similarity 88.2%; Pred. No. 2.2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGAAGGGGGTGGTGCT 19
 Db 18 AGAAGTGGGTGAGTGCT 2
 ||||| ||||| |||||

RESULT 12
 ADW43979/c
 ID ADW43979 standard; DNA; 23 BP.

XX AC ADW43979;

DT 24-MAR-2005 (first entry)

DE Human MODY 1 gene exon 4 amplifying forward primer, M1e4f3n.

XX Gene amplification; SNP detection;
 KW maturity-onset diabetes mellitus in the young; MODY gene 1; PCR; primer;
 KW ss.

XX OS Homo sapiens.

XX PN US2005003418-A1.

XX PD 06-JAN-2005.

XX PF 19-JUN-2004; 2004US-00871302.

XX PR 17-JUN-2003; 2003KR-00039125.

XX PA (KIMK/) KIM M.

XX PA (HANH/) HAN H.

XX PA (KIMS/) KIM S.

XX PA (JEON/) JEONG S.

XX PA (KIMK/) KIM K.

XX PA (LEEJ/) LEE J.

XX PA (CHOI/) CHOI Y.

XX PI Kim M, Han H, Kim S, Jeong S, Kim K, Lee J, Choi Y;

XX WPI; 2005-065236/07.

XX New primer pool including at least two sets of primers, useful for
 PT amplifying human MODY gene 1, 4, 5, 6, or 7.
 XX
 XX Claim 1; SEQ ID NO 5; 23pp; English.

XX The invention relates to a primer pool which includes at least two sets
 CC of primers for amplifying at least two target sequences of human MODY
 CC (maturity-onset diabetes mellitus in the young) gene 1, 4, 5, 6 or 7. The

CC primer pool, method and kit are useful for amplifying target sequences,
 CC specifically for amplifying human MODY gene 1, 4, 5, 6 or 7. The present
 CC sequence is a primer used to amplify human MODY gene 1 exon 4 sequence.
 XX
 SQ Sequence 23 BP; 6 A; 14 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 72.6%; Score 13.8; DB 14; Length 23;
 Best Local Similarity 88.2%; Pred. No. 2.2e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CGAGAAGGGGGTGGGTG 17
 Db 22 CGAGTAGGGGGTGGGGG 6
 ||||| ||||| |||||

RESULT 13

ADZ87881/c

ID ADZ87881 standard; RNA; 19 BP.

XX AC ADZ87881;

DT 28-JUL-2005 (first entry)

DE Early growth response gene (Egr-1) siRNA molecule #94.

XX RNA interference; gene silencing; short interfering RNA; siRNA;
 KW early growth response; Egr-1; angiogenesis disorder; cancer;
 KW breast tumor; lung tumor; bladder tumor; skin tumor; brain tumor;
 KW epithelial carcinoma; melanoma; diabetic retinopathy;
 KW age related macular degeneration; neovascular glaucoma;
 KW myopic degeneration; arthritis; psoriasis; endometriosis;
 KW gynecology and obstetrics; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; port-wine stain; Sturge-Weber syndrome;
 KW Klippel-Trenaunay-Weber syndrome; hereditary hemorrhagic telangiectasia;
 KW renal disease; polycystic kidney disease; restenosis; arteriosclerosis;
 KW cytostatic; ophthalmological; antidiabetic; antiarthritic;
 KW dermatological; virucide; cerebroprotective; vasotropic; hemostatic;
 KW osteopathic; antiangiogenic; antipapillary; antipapillary; antipapillary;
 KW antiarteriosclerotic; nephrotropic; ds.

XX OS Homo sapiens.

XX PN WO2005045032-A2.

XX PD 19-MAY-2005.

XX PF 19-AUG-2004; 2004WO-US026941.

XX PR 20-OCT-2003; 2003US-0512701P.

XX PR 23-OCT-2003; 2003US-00693059.

XX PR 24-NOV-2003; 2003US-00720448.

XX PR 03-DEC-2003; 2003US-00727780.

XX PR 14-JAN-2004; 2004US-00757803.

XX PR 10-FEB-2004; 2004US-0543480P.

XX PR 13-FEB-2004; 2004US-00780447.

XX PR 16-APR-2004; 2004US-00826966.

XX PR 30-APR-2004; 2004WO-US013456.

XX PR 24-MAY-2004; 2004WO-US016390.

XX PA (SIMA-) SIMA THERAPEUTICS INC.

XX PI Usman N, Mcswiggen J;

XX WPI; 2005-356234/36.

XX New short interfering nucleic acid molecule that directs cleavage of an
 PT early growth response RNA, useful for treating cancer, ocular disease,
 PT proliferative condition, renal disease or arteriosclerosis.
 XX
 XX Claim 33; SEQ ID NO 94; 200pp; English.

XX The invention relates to a chemically synthesized double stranded short
 CC interfering nucleic acid (siRNA) molecule that directs cleavage of an

CC early growth response (Egr-1) RNA via RNA interference (RNAi). The
CC invention also relates to a composition comprising the siRNA molecule with
CC a pharmaceutical carrier or diluent. The siRNA molecule is useful for
CC treating tumor angiogenesis and cancer, e.g., breast, lung, bladder,
CC skin, and brain cancer, epithelial carcinoma, and melanoma. The molecule
CC is also useful for treating diabetic retinopathy, age related macular
CC degeneration, neovascular glaucoma, myopic degeneration, arthritis,
CC psoriasis, endometriosis, female reproductive disorders, verruca
CC vulgaris, angiofibroma, tuberosus sclerosis, port-wine stains, Sturge-
CC Weber syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu
CC syndrome, renal disease, polycystic kidney disease, restenosis and
CC arteriosclerosis. This sequence represents an Egr-1 siRNA molecule of the
CC invention.

XX SQ Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGG 15

DB 19 GGAGAGGGGGTGGG 5

RESULT 14

ID ADZ88055 standard; RNA; 19 BP.

AC ADZ88055;

XX 28-JUL-2005 (first entry)

XX

DE Early growth response gene (Egr-1) siRNA molecule #268.

XX

XX RNA interference; gene silencing; short interfering RNA; siRNA;
KW early growth response; Egr-1; angiogenesis disorder; cancer;
KW breast tumor; lung tumor; bladder tumor; skin tumor; brain tumor;
KW epithelial carcinoma; melanoma; diabetic retinopathy;
KW age related macular degeneration; neovascular glaucoma;
KW myopic degeneration; arthritis; psoriasis; endometriosis;
KW gynecology and obstetrics; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; port-wine stain; Sturge-Weber syndrome;
KW Klippel-Trenaunay-Weber syndrome; hereditary hemorrhagic telangiectasia;
KW renal disease; polycystic kidney disease; restenosis; arteriosclerosis;
KW cytoskeletal; ophthalmological; antidiabetic; antiarthritic;
KW dermatological; virucide; cerebroprotective; vasotrophic; hemostatic;
KW osteopathic; antiangiogenic; antipsoriatic; gynecological;
KW antiarteriosclerotic; nephrotropic; ds.

XX Homo sapiens.

XX WO2005045032-A2.

XX 19-MAY-2005.

XX

XX 19-AUG-2004; 2004WO-US026941.

XX

XX 20-OCT-2003; 2003US-0512701P.

XX

XX 23-OCT-2003; 2003US-00693059.

XX

XX 24-NOV-2003; 2003US-00720448.

XX

XX 03-DEC-2003; 2003US-00727780.

XX

XX 14-JAN-2004; 2004US-00757803.

XX

XX 10-FEB-2004; 2004US-0543480P.

XX

XX 13-FEB-2004; 2004US-00780447.

XX

XX 16-APR-2004; 2004US-00826966.

XX

XX 30-APR-2004; 2004WO-US013456.

XX

XX 24-MAY-2004; 2004WO-US016390.

DR WPI; 2005-356234/36.

XX New short interfering nucleic acid molecule that directs cleavage of an
XX early growth response RNA, useful for treating cancer, ocular disease,
XX proliferative condition, renal disease or arteriosclerosis.

PS Claim 33; SEQ ID NO 268; 200pp; English.

XX The invention relates to a chemically synthesized double stranded short
XX interfering nucleic acid (siRNA) molecule that directs cleavage of an
XX early growth response (Egr-1) RNA via RNA interference (RNAi). The
XX invention also relates to a composition comprising the siRNA molecule with
XX a pharmaceutical carrier or diluent. The siRNA molecule is useful for
XX treating tumor angiogenesis and cancer, e.g., breast, lung, bladder,
XX skin, and brain cancer, epithelial carcinoma, and melanoma. The molecule
XX is also useful for treating diabetic retinopathy, age related macular
XX degeneration, neovascular glaucoma, myopic degeneration, arthritis,
XX psoriasis, endometriosis, female reproductive disorders, verruca
XX vulgaris, angiofibroma, tuberosus sclerosis, port-wine stains, Sturge-
XX Weber syndrome, Klippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu
XX syndrome, renal disease, polycystic kidney disease, restenosis and
XX arteriosclerosis. This sequence represents an Egr-1 siRNA molecule of the
XX invention.

SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;

Best Local Similarity 86.7%; Pred. No. 3.3e+04;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGG 15

DB 1 GGAGAGGGGGTGGG 15

RESULT 15

AEBA43635

ID AEB43635 standard; RNA; 19 BP.

XX AEB43635;

AC AEB43635;

XX 22-SEP-2005 (first entry)

XX

DE Novel human Egr-1 gene-targeting siRNA sequence SeqID268.

XX

XX antiarthritic; vasotropic; antiinflammatory; ophthalmological;
KW antidiabetic; antipsoriatic; cerebroprotective; antiarteriosclerotic;
KW cancer; ocular disease; tumor; angiogenesis; angiogenesis;
KW hyperproliferation; diabetic retinopathy; macular degeneration; aging;
KW arthritis; psoriasis; sturge-weber syndrome; restenosis;
KW arteriosclerosis; RNA interference; gene silencing;
KW short interfering RNA; siRNA; cytoskeletal; drug screening; diagnostic;
KW genetic engineering; gene mapping; Egr-1; ss.

XX Homo sapiens.

XX OS

XX US2005153915-A1.

XX

XX 14-JUL-2005.

XX

XX 19-AUG-2004; 2004US-00922544.

XX

XX 18-MAY-2001; 2001US-0292217P.

XX

XX 20-JUL-2001; 2001US-0306883P.

XX

XX 13-AUG-2001; 2001US-0311865P.

XX

XX 20-FEB-2002; 2002US-0358580P.

XX

XX 06-MAR-2002; 2002US-0362016P.

XX

XX 11-MAR-2002; 2002US-0363124P.

XX

XX 20-MAY-2002; 2002WO-US015876.

XX

XX 06-JUN-2002; 2002US-0386782P.

XX

XX 29-AUG-2002; 2002US-0406784P.

PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 23-MAY-2003; 2003US-0044853.
PR 20-OCT-2003; 2003US-0512703P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX Usman N, Mcswiggen J;
XX WPI; 2005-505469/51.
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of early growth response-1 RNA by RNA
PT interference, useful in treating cancer, ocular disease or restenosis.
XX Claim 33; SEQ ID NO 268; 218pp; English.
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of the Egr-1 gene by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising a siRNA targeted to the Human Egr-1 mRNA. The
CC invention further discloses expression vectors and host cells comprising
CC a siRNA of the invention. The siRNAs are used to modulate expression of
CC the Egr-1 gene in cells, tissue explants or organisms (for example by ex
CC vivo gene therapy), or in grafts and transplants for the treatment of a
CC variety of conditions. The siRNAs may be useful for the development of
CC compounds with a cytostatic, antiarthritic, vasotropic, antiinflammatory,
CC ophthalmological, antidiabetic, antipsoriatic, cerebroprotective or
CC antiarteriosclerotic activity acting by RNA interference. They may be
CC used in the treatment of cancer (for example colorectal cancer,
CC adenocarcinoma, lymphoma and glioma), ocular disease (for example toxic
CC conjunctivitis, bacterial keratitis, uveitis glaucoma and squamous cell
CC carcinoma), tumor angiogenesis, and proliferative conditions such as
CC diabetic retinopathy, macular degeneration, age related macular
CC degeneration, arthritis, psoriasis, Sturge Weber syndrome, restenosis
CC and/or arteriosclerosis. The siRNAs may also be used in drug screening,
CC diagnosis, therapeutic target identification and validation, genetic
CC engineering, pharmacogenomics, studying gene function and gene mapping
CC (for example of single nucleotide polymorphisms). The present sequence is
CC that of a human Egr-1 gene-targeting siRNA of the invention.
XX SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;
Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 86.7%; Pred. NO. 3.3e+04;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGAGAGGGGGTGGG 15
||||| :|||
DB 1 CGAGAGGGGGTGGG 15
RESULT 16
AEB43461/c
ID AEB43461 standard; RNA; 19 BP.
XX

AC AEB43461;
XX 22-SEP-2005 (first entry)
XX Novel human Egr-1 gene-targeting siRNA sequence SeqID94.
XX antiarthritic; vasotropic; antiinflammatory; ophthalmological;
KW antidiabetic; antipsoriatic; cerebroprotective; antiarteriosclerotic;
KW cancer; ocular disease; tumor; angiogenesis; angiogenesis;
KW hyperproliferation; diabetic retinopathy; macular degeneration; aging;
KW arthritis; psoriasis; sturge-weber syndrome; restenosis;
KW arteriosclerosis; RNA interference; gene silencing;
KW short interfering RNA; siRNA; cytostatic; drug screening; diagnostic;
KW genetic engineering; gene mapping; Egr-1; ss.
XX Homo sapiens.
XX US2005153915-A1.
XX 14-JUL-2005.
XX 19-AUG-2004; 2004US-00922544.
XX 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 20-FEB-2003; 2003WO-US005028.
PR 30-APR-2003; 2003WO-US005346.
PR 23-MAY-2003; 2003US-0044853.
PR 20-OCT-2003; 2003US-0512701P.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX Usman N, Mcswiggen J;
XX WPI; 2005-505469/51.
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of early growth response-1 RNA by RNA
PT interference, useful in treating cancer, ocular disease or restenosis.
XX Claim 33; SEQ ID NO 94; 218pp; English.
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of the Egr-1 gene by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising a siRNA targeted to the Human Egr-1 mRNA. The
CC invention further discloses expression vectors and host cells comprising

an siNA of the invention. The siNAs are used to modulate expression of the Egr-1 gene in cells, tissue explants or organisms (for example by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. The siRNAs may be useful for the development of compounds with a cytostatic, antiarthritic, vasotropic, antiinflammatory, ophthalmological, antidiabetic, antipsoriatic, cerebroprotective or antiarteriosclerotic activity acting by RNA interference. They may be used in the treatment of cancer (for example colorectal cancer, adenocarcinoma, lymphoma and glioma), ocular disease (for example toxic conjunctivitis, bacterial keratitis, uveitic glaucoma and squamous cell carcinoma), tumor angiogenesis, and proliferative conditions such as diabetic retinopathy, macular degeneration, age related macular degeneration, arthritis, psoriasis, Sturge Weber syndrome, restenosis and/or arteriosclerosis. The siNAs may also be used in drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single nucleotide polymorphisms). The present sequence is that of a human Egr-1 gene-targeting siRNA of the invention.

SQ Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.3e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15

Db 19 GGAGAGGGGGTGGG 5

RESULT 17

AA045780/c

ID AA045780 standard; DNA; 22 BP.

XX AC AA045780;

XX DT 27-DEC-2002 (first entry)

XX DE Human promoter -147 CYP4503A5 specific probe #1.

XX KW Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase; polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent; drug-drug interaction; drug adverse effect; anti-cancer agent; enzyme; probe; promoter; ss.

XX OS Homo sapiens.

XX PN WO200268448-A1.

XX PD 06-SEP-2002.

XX PF 26-FEB-2002; 2002WO-US006135.

XX PR 26-FEB-2001; 2001US-0271630P.

XX PA (DNAS-) DNA SCI INC.

XX PA (UYDU-) UNIV DUKE.

XX PI Guida M, Hall J, Petros WP, Vredenburg JJ, Colvin OM, Marks JR;

XX DR WPI; 2002-691652/74.

XX PT New nucleic acid molecule useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer treatments, comprises at least one base variation from human CYP3A4 or CYP3A5 sequence.

XX PS Example 3; Page 27; 41pp; English.

XX CC The invention relates to a nucleic acid molecule comprising at least one base variation from human cytochrome P450 (CYP) 3A4 or CYP3A5 sequence. Nucleic acid molecules of the invention are useful for identifying polymorphisms associated with CYP3A4, CYP3A5 or glutathione S-transferase

CC (GST) M1 substrates which influence breast cancer treatments. They are also useful in diagnostic purposes to identify individuals having a polymorphic genotype which influence the outcome of breast cancer treatments and the selection of chemotherapeutic agents used to treat breast cancer. The polymorphisms detected are used to screen altered metabolism of CYP3A4, CYP3A5 or GSTM1 substrates, potential drug-drug interactions, drug adverse effects, likelihood of successful clinical outcome following treatment with anti-cancer agents such as cisplatin, cyclophosphamide and/or BCNU. The present sequence is human promoter -147 CYP4503A5 specific probe

XX SQ Sequence 22 BP; 2 A; 13 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 70.5%; Score 13.4; DB 6; Length 22;

Best Local Similarity 93.3%; Pred. No. 3.3e+04;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15

Db 22 GGAGAGGGGGTGGG 8

RESULT 18

AAZ75471/c

ID AAZ75471 standard; DNA; 18 BP.

XX AC AAZ75471;

XX DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO:9827.

XX KW Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; amplification; single nucleotide polymorphism; SNP; PCR primer; diagnosis; ss.

XX OS Homo sapiens.

XX PN WO9954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 99WO-IB000822.

XX PR 21-APR-1998; 98US-0082614P.

XX PR 23-NOV-1998; 98US-0109732P.

XX PA (GEST) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium map of the human genome.

XX PS Claim 8; Page 2325; 2745pp; English.

XX CC AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

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CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 18 BP; 3 A; 8 C; 1 G; 6 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAAGGGGGTGGGTGCT 19
   ||||| ||| |||||
DB 18 GAGAAAGGGTAAAGTCT 1

RESULT 19
ADI57107/c
ID ADI57107 standard; DNA; 20 BP.
XX
AC ADI57107;
XX
XX 22-APR-2004 (first entry)
XX
DE Oryza minuta Pi9 locus nucleotide binding site (NBS) gene PCR primer #24.
XX
KW nucleotide binding site; NBS; Pi9 gene; bacterial blight; rice blast;
KW plant breeding; transgenic plant; plant; PCR; primer; ss.
XX
OS Oryza minuta.
XX
PN US2004006788-A1.
XX
PD 08-JAN-2004.
XX
PF 27-JAN-2003; 2003US-00352179.
XX
XX 25-JAN-2002; 2002US-0352108P.
PR 01-FEB-2002; 2002US-0353304P.
XX
XX (WANG/) WANG G.
PA (LIU/) LIU G.
XX
XX Wang G, Liu G;
XX
XX WPI; 2004-121064/12.
DR
PT Nucleic acids encoding nucleotide binding site (NBS) proteins NBS1, NBS2
PT and NBS3, useful for producing plants resistant to Magnaporthe grisea
PT infection.
XX
PS Disclosure; SEQ ID NO 24; 136pp; English.
XX
CC The invention comprises the amino acid and coding sequences of nucleotide
CC binding site (NBS) proteins from the Oryza minuta Pi9 locus (bacterial
CC blight and rice blast resistance genes). The DNA sequences may be used as
CC markers for resistance to infection with Magnaporthe grisea in plant
CC breeding programs. The present DNA sequence represents a PCR primer for
CC the Oryza minuta Pi9 locus.
XX
XX Sequence 20 BP; 6 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 12; Length 20;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAAGGGGGTGGGTGCT 19
   ||||| ||| |||||
DB 20 GAGATGGTGGTGGCTGCT 3

RESULT 20
ABA00323
ID ABA00323 standard; cDNA; 21 BP.
XX
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AC ABA00323;
XX
XX 09-DEC-2002 (first entry)
XX
DE cDNA encoding TCR beta-chain N-D-N junction region from donor UA.
XX
KW Transcription factor; STAT-1; monocyte; unstable angina; UA;
KW stable angina; SA; SIE oligonucleotide; sis-inducible element;
KW interferon; IFN-gamma; unstable plaque; cardiovascular condition; angina;
KW PCR; primer; amplify; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 1..21
FT /*tag= a
FT /*partial
XX
PN WO200267766-A2.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002WO-US005760.
XX
XX 23-FEB-2001; 2001US-00792686.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Goronzy JJ, Weyand CM, Kopecky SL;
XX
XX WPI; 2002-698620/75.
DR P-PSDB; AAG79536.
XX
XX Determining whether or not a mammal has an unstable plaque, useful for
XX evaluating the severity of cardiovascular conditions, e.g. angina,
XX comprises determining the level of CD64 or IP-10 polypeptide encoded by
XX DNA responsive to STAT-1.
XX
XX Example 8; Page 29; 49pp; English.
XX
XX The sequences given in ABA00318-27 are sequences which encode the N-D-N
XX junction region at the interface of TCR-BV and -BJ gene segments in
XX unstable angina (UA) patients. All these sequences have shared amino acid
XX sequence homology and display heterogeneity at the nucleotide level.
XX Sequences like these were identified using the method of the invention
XX for determining if a mammal has an unstable plaque. The method comprises
XX determining whether or not a sample from the mammal contains an elevated
XX level of a polypeptide which is encoded by a DNA responsive to an
XX interferon-gamma-activated transcription factor. The level indicates that
XX the mammal contains the unstable plaque. The method is useful in
XX evaluating the severity of cardiovascular conditions, such as angina,
XX specifically by determining whether a person has an unstable plaque. The
XX method may also be used to identify compounds that are useful in treating
XX or reducing the risk of developing life-threatening cardiovascular
XX conditions
XX
XX Sequence 21 BP; 3 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match          69.5%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAAGGGGGTGGGTGCT 19
   ||||| ||| |||||
DB 2 GCGAAGGGGGGGGGTCT 19

RESULT 21
AAV72586
ID AAV72586 standard; DNA; 25 BP.
XX
XX AAV72586;
XX
```

DT 15-MAR-1999 (first entry)
XX NOXR1 cDNA specific primer IIA.
DE
XX NOXR1; antimicrobial resistance; tuberculosis; macrophage; vaccine;
KW septic hypotension; stroke; therapy; PCR; primer; ss.
KW
XX Synthetic.
OS Mycobacterium tuberculosis.
OS
XX WO9850402-A1.
FN
XX 12-NOV-1998.
PD
XX 28-APR-1998; 98WO-US008497.
PF
XX 06-MAY-1997; 97US-0045688P.
PR
XX (CORR) CORNELL RES FOUND INC.
PA
XX Riley LW, Nathan CF, Ehrh S;
PI
XX WPI; 1999-034703/03.
DR
XX DNA conferring resistance on Mycobacterium tuberculosis - to
PT antimicrobial reactive oxygen and nitrogen intermediates, used for
PT vaccinating mammals against Mycobacterium.
XX
XX Example 8; Page 29; 80pp; English.
PS
XX This is the nucleotide sequence of primer IIA that is specific for NOXR1
CC cDNA (see AAU72577) of Mycobacterium tuberculosis. Primer sets Ia and Ib
CC (see AAU72584-85), and IIA and IIB (see AAU72587), were used in RT-PCR to
CC demonstrate expression of recombinant NOXR1 in Mycobacterium smegmatis
CC and of native NOXR1 in M. tuberculosis. NOXR1 confers resistance to
CC antibacterial reactive nitrogen and oxygen intermediates. NOXR1 nucleic
CC acids, polypeptides (see AAU83357) and antibodies can be used in the
CC production of vaccines, in diagnostic methods, and in methods for
CC treating septic hypotension and stroke, and for quenching overproduction
CC of nitric oxide in response to infection
XX
XX Sequence 25 BP; 1 A; 3 C; 16 G; 5 T; 0 U; 0 Other;
SQ
Query Match 69.5%; Score 13.2; DB 2; Length 25;
Best Local Similarity 83.3%; Pred. NO. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAGAGGGGGTGGGTGC 18
DB 1 GGGGATGGCGTGGGTGC 18
RESULT 22
ADO12772/c
ID ADO12772 standard; DNA; 30 BP.
XX
XX ADO12772;
AC
XX 15-JUL-2004 (first entry)
DT
XX Single multiplex PCR primer #2144.
DE
XX ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
KW gene expression profiling.
XX
XX Synthetic.
OS
XX WO2004033649-A2.
FN
XX 22-APR-2004.
PD
XX

PF 07-OCT-2003; 2003WO-US031874.
XX
XX 07-OCT-2002; 2002US-0417009P.
PR
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA
XX Li H, Li J;
PI
XX WPI; 2004-340914/31.
DR
XX Designing primers for simultaneous amplification of target DNA fragments
XX in a single multiplex polymerase chain reaction, for high throughput
PT multiplex DNA sequence amplification, comprises aligning two primers.
PT
XX Disclosure; Page 43; 120pp; English.
PS
XX The invention relates to a method of designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction by aligning a first primer and a second primer. The method
CC comprises: (a) aligning a first primer and a second primer; and (b)
CC selecting the first primer where the first primer at its 3' end does not
CC contain four or more bases that are perfectly matching to the 3' end
CC sequence of the first primer or a second primer, the first primer at its
CC 3' end does not contain seven or more bases that are perfectly matching
CC except one mismatch to the 3' end sequence of the first primer or the
CC second primer, the first primer at its 3' end does not contain six or
CC more bases that are perfectly matching to a sequence anywhere of the
CC first primer or the second primer, and the first primer at its 3' end
CC does not contain eleven or more bases that are perfectly matching except
CC one mismatch to a sequence anywhere of the first primer or the second
CC primer. The method is useful for designing primers for simultaneous
CC amplification of target DNA fragments in a single multiplex polymerase
CC chain reaction. It is also useful in the identification of multiple genes
CC related to multifactorial diseases, the genome-scale detection of genetic
CC alterations, the studies in pharmacogenetic reactions, the genotyping
CC genetic polymorphisms in a large population, the gene expression
CC profiling in various samples and high throughput genotyping technologies.
XX This sequence corresponds to an example of a primer of the invention.
XX
XX Sequence 30 BP; 5 A; 10 C; 4 G; 11 T; 0 U; 0 Other;
SQ
Query Match 69.5%; Score 13.2; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. NO. 4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GAGAGGGGGTGGGTGCT 19
DB 19 GAGAGGGGATAGGTGCT 2
RESULT 23
ADO12782
ID ADO12782 standard; DNA; 30 BP.
XX
XX ADO12782;
AC
XX 15-JUL-2004 (first entry)
DT
XX Single multiplex PCR primer #2154.
DE
XX ss; primer; simultaneous amplification;
KW single multiplex polymerase chain reaction; multifactorial disease;
KW genetic alteration; pharmacogenetic reaction; genotyping; polymorphism;
KW gene expression profiling.
XX
XX Synthetic.
OS
XX WO2004033649-A2.
FN
XX 22-APR-2004.
PD
XX 07-OCT-2003; 2003WO-US031874.
PF
XX

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PR 07-OCT-2002; 2002US-0417009P.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Li H, Li J;
XX WPI; 2004-340914/31.
XX Designing primers for simultaneous amplification of target DNA fragments
XX in a single multiplex polymerase chain reaction, for high throughput
XX multiplex DNA sequence amplification, comprises aligning two primers.
XX Disclosure; Page 43; 120pp; English.
XX The invention relates to a method of designing primers for simultaneous
XX amplification of target DNA fragments in a single multiplex polymerase
XX chain reaction by aligning a first primer and a second primer. The method
XX comprises: (a) aligning a first primer and a second primer; and (b)
XX selecting the first primer where the first primer at its 3' end does not
XX contain four or more bases that are perfectly matching to the 3' end
XX sequence of the first primer or a second primer, the first primer at its
XX 3' end does not contain seven or more bases that are perfectly matching
XX except one mismatch to the 3' end sequence of the first primer or the
XX second primer, the first primer at its 3' end does not contain six or
XX more bases that are perfectly matching to a sequence anywhere of the
XX first primer or the second primer, and the first primer at its 3' end
XX does not contain eleven or more bases that are perfectly matching except
XX one mismatch to a sequence anywhere of the first primer or the second
XX primer. The method is useful for designing primers for simultaneous
XX amplification of target DNA fragments in a single multiplex polymerase
XX chain reaction. It is also useful in the identification of multiple genes
XX related to multifactorial diseases, the genome-scale detection of genetic
XX alterations, the studies in pharmacogenetic reactions, the genotyping
XX genetic polymorphisms in a large population, the gene expression
XX profiling in various samples and high throughput genotyping technologies.
XX This sequence corresponds to an example of a primer of the invention.
XX Sequence 30 BP; 11 A; 4 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 69.5%; Score 13.2; DB 12; Length 30;
Best Local Similarity 83.3%; Pred. No. 4e+04; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 3;
QY 2 GAGAGGGGGTGGGTCT 19
Db 12 GAGAGGGGATAGGGTCT 29
|||||
RESULT 24
ABC22092
ID ABC22092 standard; DNA; 13 BP.
XX AC ABC22092;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 22109 for detecting SNP TSC0004396.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 22110; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF0010-ABF99989, ABH0010-ABH99989 and AB100010-AB182073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 13 BP; 3 A; 0 C; 9 G; 1 T; 0 U; 0 Other;
Query Match 68.4%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+04; Mismatches 0; Gaps 0;
Matches 13; Conservative 0; Indels 0;
QY 3 AGAAGGGGGTGGG 15
Db 1 AGAAGGGGGTGGG 13
|||||
RESULT 25
ABC22093/c
ID ABC22093 standard; DNA; 13 BP.
XX AC ABC22093;
XX 20-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 22110 for detecting SNP TSC0004396.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 22110; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
```


CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 13 BP; 1 A; 9 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 68.4%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
|||||
Db 13 AGAAGGGGGTGGG 1

RESULT 26

AAQ99298/c
ID AAQ99298 standard; cDNA; 20 BP.

XX AC AAQ99298;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1112.

XX KW Antisense oligonucleotide; nucleotides 1710-1729 and 3639-3658;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.

XX OS Synthetic.

XX FN WO9602556-A2.

XX PD 01-FEB-1996.

XX PF 18-JUL-1995; 95WO-US009011.

XX PR 18-JUL-1994; 94US-00276567.

XX FA (HYBR-) HYBRIDON INC.

XX PI Smyth AP;

XX DR WPI; 1996-105848/11.

XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
XX preventing induction of multi:drug resistance or for treating multi:drug
XX resistant cancer cells.

XX PS Claim 9; Page 14; 43pp; English.

XX CC The present oligonucleotide is antisense to nucleotides 1710-1729 and
CC 3639-3658 of the multi-drug resistant-1 (MDR-1) gene, which encode the
CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
CC oligonucleotide inhibits the expression of P170, and can therefore be
CC used to treat MDR cancer cells, and prevent the induction of MDR in
CC cancer cells and the expression of P170 in cells

XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTG 17

Db 18 GAGAAGGGGTGCGGTG 3
|||||

RESULT 27

AAQ99297/c

ID AAQ99297 standard; cDNA; 20 BP.

XX AC AAQ99297;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1111.

XX KW Antisense oligonucleotide; nucleotides 1709-1729 and 3638-3657;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.

XX OS Synthetic.

XX FN WO9602556-A2.

XX PD 01-FEB-1996.

XX PF 18-JUL-1995; 95WO-US009011.

XX PR 18-JUL-1994; 94US-00276567.

XX FA (HYBR-) HYBRIDON INC.

XX PI Smyth AP;

XX DR WPI; 1996-105848/11.

XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
XX preventing induction of multi:drug resistance or for treating multi:drug
XX resistant cancer cells.

XX PS Claim 8; Page 14; 43pp; English.

XX CC The present oligonucleotide is antisense to nucleotides 1709-1729 and
CC 3638-3657 of the multi-drug resistant-1 (MDR-1) gene, which encode the
CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
CC oligonucleotide inhibits the expression of P170, and can therefore be
CC used to treat MDR cancer cells, and prevent the induction of MDR in
CC cancer cells and the expression of P170 in cells

XX SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTG 17
|||||

Db 17 GAGAAGGGGTGCGGTG 2
|||||

RESULT 28

AAQ99296/c

ID AAQ99296 standard; cDNA; 20 BP.

XX AC AAQ99296;

XX DT 06-SEP-1996 (first entry)

XX DE Multi-drug resistant-1 gene antisense oligonucleotide 1110.

XX KW Antisense oligonucleotide; nucleotides 1708-1727 and 3637-3656;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.

XX OS Synthetic.
XX PN WO9602556-A2.
XX PD 01-FEB-1996.
XX PF 18-JUL-1995; 95WO-US009011.
XX PR 18-JUL-1994; 94US-00276567.
XX PA (HYBR-) HYBRIDON INC.
XX PI Smyth AP;
XX DR WPI; 1996-105848/11.
XX PT New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
PT preventing induction of multi:drug resistance or for treating multi:drug
PT resistant cancer cells.
XX PS Claim 7; Page 14; 43pp; English.
XX CC The present oligonucleotide is antisense to nucleotides 1708-1727 and
CC 3637-3656 of the multi-drug resistant-1 (MDR-1) gene, which encode the
CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
CC oligonucleotide inhibits the expression of P170, and can therefore be
CC used to treat MDR cancer cells, and prevent the induction of MDR in
CC cancer cells and the expression of P170 in cells
XX Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
SQ Query Match 67.4%; Score 12.8; DB 2; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGGGTGGGTG 17
DB 16 GAGAGGGGTGCGGTG 1
RESULT 29
AAD48534
ID AAD48534 standard; DNA; 20 BP.
XX AC AAD48534;
XX DT 24-FEB-2003 (first entry)
XX DE Chicken lysozyme gene fragment sequencing PCR primer, lys033for.
XX KW Lysozyme gene expression control region; chromosomal positional effect;
XX KW transgene; avian cell; PCR; primer; chicken; ss.
XX OS Gallus sp.
XX PN WO200279447-A2.
XX PD 10-OCT-2002.
XX PF 29-MAR-2002; 2002WO-US009866.
XX PR 30-MAR-2001; 2001US-0280004P.
XX PR 03-AUG-2001; 2001US-00922549.
XX PR 25-JAN-2002; 2002US-0351550P.
XX PA (AVIG-) AVIGENICS INC.
XX PI Rapp JC;
XX DR WPI; 2003-046807/04.
XX PT New isolated or recombinant nucleic acid for reducing the chromosomal

PT positional effect of a transgene, comprises an isolated avian lysozyme
PT gene expression control region.
XX Example 1; Fig 1; 88pp; English.
XX CC The invention relates to an isolated or recombinant nucleic acid or DNA
CC molecule comprising an isolated avian lysozyme gene expression control
CC region operably linked to a nucleic acid insert encoding a polypeptide.
CC The nucleic acid is useful for reducing the chromosomal positional effect
CC of a transgene operably linked to the lysozyme gene expression control
CC region and transfected into a recipient avian cell. The present sequence
CC is a PCR primer used for sequencing chicken lysozyme gene expression
CC control region
XX Sequence 20 BP; 3 A; 0 C; 11 G; 6 T; 0 U; 0 Other;
SQ Query Match 67.4%; Score 12.8; DB 8; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGGGTGGGTG 17
DB 1 GAGAGGGGGTGGGTG 16
RESULT 30
ACC59333
ID ACC59333 standard; DNA; 20 BP.
XX AC ACC59333;
XX DT 08-SEP-2003 (first entry)
XX DE Human MIZIP coding sequence fragment #5.
XX KW Zinc finger protein; MCH-R; MCH receptor; anorectic; appetite disorder;
XX KW melanin concentrating hormone receptor interacting protein; gene; db.
XX OS Homo sapiens.
XX PN WO2003042242-A1.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-EP012714.
XX PR 14-NOV-2001; 2001DE-01055841.
XX PA (UYHA-) UNIV HAMBURG-EPPENDORF.
XX PI Richter D, Baechner D, Kreienkamp H;
XX DR WPI; 2003-468631/44.
XX PT New polynucleotide encoding melanin-concentrating hormone receptor
XX PT interacting protein, useful for diagnosis of appetite disorders and to
XX PT screen for appetite regulators.
XX PS Disclosure; Fig 4C; 71pp; German.
XX CC The present invention provides the protein and coding sequences of human
XX CC melanin concentrating hormone receptor (MCH-R) interacting protein. The
XX CC sequences can be used in the production of transgenic animals useful for
XX CC studying appetite disorders and treatments. The present sequence is a
XX CC coding sequence shown in the exemplification of the invention
XX SQ Sequence 20 BP; 4 A; 2 C; 10 G; 4 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 9; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAGGGGGTGGGTG 17

```
Db          ||||||| |||||||
            2 GAGAGCAGGTGGTG 17

RESULT 31
ADK23418
ID ADK23418 standard; DNA; 20 BP.
XX
AC ADK23418;
XX
DT 18-NOV-2004 (first entry)
XX
DE Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3495.
XX
KW acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
KW metabolic syndrome X; cardiovascular disorder; cancer; infection;
KW inflammation; tumour; antisense; ss.
XX
OS Synthetic.
XX
PN WO2004016749-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025389.
XX
PR 14-AUG-2002; 2002US-0403591P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Ross SA;
XX
DR WPI; 2004-203782/19.
XX
PT New antisense compounds targeted to nucleic acid molecules encoding acyl-
PT coenzyme A synthetase 1 (ACS1), useful for treating diseases or
PT conditions associated with aberrant expression of ACS1, e.g. diabetes,
PT obesity or cancer.
XX
PS Claim 3; SEQ ID NO 3495; 940pp; English.
XX
CC The invention relates to an antisense compound targeted to a nucleic acid
CC molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense
CC compound specifically hybridises with and inhibits the expression of
CC ACS1. The antisense oligonucleotides or compounds are useful for
CC inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for
CC treating diseases or conditions associated with aberrant expression of
CC ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular
CC disorder or cancer. The antisense compounds are also useful as research
CC reagents and kits, or in diagnostic, therapeutic and prophylactic
CC applications, e.g. to prevent or delay infection, inflammation or tumour
CC formation. The present sequence represents an acyl-coenzyme A synthetase
CC 1, ACS1, antisense oligonucleotide.
XX
SQ Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 13; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAAGGGGGTGGGTGCT 19
    ||||| |||||
Db 1 GAAGGTGGTGGTGCT 16

RESULT 32
ADK23492
ID ADK23492 standard; DNA; 20 BP.
XX
AC ADK23492;
XX
DT 18-NOV-2004 (first entry)
XX

Acyl-coenzyme A synthetase 1, ACS1, antisense oligonucleotide #3569.
acyl-coenzyme A synthetase 1; ACS1; diabetes; obesity;
metabolic syndrome X; cardiovascular disorder; cancer; infection;
inflammation; tumour; antisense; ss.
Synthetic.
WO2004016749-A2.
26-FEB-2004.
14-AUG-2003; 2003WO-US025389.
14-AUG-2002; 2002US-0403591P.
(PHAA ) PHARMACIA CORP.
Ross SA;
WPI; 2004-203782/19.
New antisense compounds targeted to nucleic acid molecules encoding acyl-
coenzyme A synthetase 1 (ACS1), useful for treating diseases or
conditions associated with aberrant expression of ACS1, e.g. diabetes,
obesity or cancer.
Claim 3; SEQ ID NO 3569; 940pp; English.
The invention relates to an antisense compound targeted to a nucleic acid
molecule encoding acyl-coenzyme A synthetase 1 (ACS1). The antisense
compound specifically hybridises with and inhibits the expression of
ACS1. The antisense oligonucleotides or compounds are useful for
inhibiting the expression of acyl-coenzyme A synthetase 1 (ACS1), and for
treating diseases or conditions associated with aberrant expression of
ACS1, e.g. diabetes, obesity, metabolic syndrome X, cardiovascular
disorder or cancer. The antisense compounds are also useful as research
reagents and kits, or in diagnostic, therapeutic and prophylactic
applications, e.g. to prevent or delay infection, inflammation or tumour
formation. The present sequence represents an acyl-coenzyme A synthetase
1, ACS1, antisense oligonucleotide.
Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 67.4%; Score 12.8; DB 13; Length 20;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGTGC 18
    ||||| |||||
Db 5 AGAAGGTGGTGGGTGC 20

RESULT 33
AAQ99295/c
ID AAQ99295 standard; cDNA; 22 BP.
XX
AC AAQ99295;
XX
DT 06-SEP-1996 (first entry)
XX
DE Multi-drug resistant-1 gene antisense oligonucleotide 707.
XX
KW Antisense oligonucleotide; nucleotides 1708-1729 and 3637-3658;
KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;
KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;
KW induction; prevention; ss.
XX
OS Synthetic.
XX
PN WO9602556-A2.
XX
PD 01-FEB-1996.
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XX 18-JUL-1995; 95WO-US009011.
 XX PF
 XX 18-JUL-1994; 94US-00276567.
 XX PR
 XX (HYBR-) HYBRIDON INC.
 XX PA
 XX Smyth AP;
 XX PI
 XX WPI; 1996-105848/11.
 XX DR
 XX New oligo:nucleotide(s) complementary to the MDR-1 gene - used for
 XX PT preventing induction of multi:drug resistance or for treating multi:drug
 XX PT resistant cancer cells.
 XX PT
 XX Claim 6; Page 14; 43pp; English.
 XX PS
 XX The present oligonucleotide is antisense to nucleotides 1708-1729 and
 XX CC 3637-3658 of the multi-drug resistant-1 (MDR-1) gene, which encode the
 XX CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The
 XX CC oligonucleotide inhibits the expression of P170, and can therefore be
 XX CC used to treat MDR cancer cells, and prevent the induction of MDR in
 XX CC cancer cells and the expression of P170 in cells
 XX CC
 XX Sequence 22 BP; 3 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
 SQ

Query Match 67.4%; Score 12.8; DB 2; Length 22;
 Best Local Similarity 87.5%; Pred. No. 5.9e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GAGAAAGGGGTGGGTG 17
 |||||
 DB 18 GAGAAAGGGGTGGGTG 3

RESULT 34
 ADY33449
 ID ADY33449 standard; DNA; 23 BP.
 XX AC
 XX ADY33449;
 XX DT
 XX 05-MAY-2005 (first entry)
 XX DE
 XX CFTR gene mutation/polymorphism detection primer, SEQ ID 716.
 XX KW mutation; SNP detection; cystic fibrosis; primer; PCR; ss.
 XX OS Synthetic.
 XX WO2005016251-A2.
 XX PN
 XX 24-FEB-2005.
 XX PD
 XX 12-JUL-2004; 2004WO-US022376.
 XX PF
 XX 10-JUL-2003; 2003US-0486864P.
 XX PR
 XX (AMBR-) AMERY GENETICS CORP.
 XX PA
 XX Dunlop CLM, Kammescheidt A;
 XX PI
 XX WPI; 2005-182207/19.
 XX DR
 XX Identifying presence/absence of mutation or polymorphism in cystic
 XX PT fibrosis transmembrane conductance regulator gene, by contacting nucleic
 XX PT acid and primer set, producing extension product, analyzing product for
 XX PT mutation or polymorphism.
 XX XX
 XX Claim 1; SEQ ID NO 849; 313pp; English.
 XX PS
 XX The invention relates to a novel method for identifying the
 XX CC presence/absence of a mutation or polymorphism in the cystic fibrosis
 XX CC transmembrane conductance regulator (CFTR) gene of subject. The method

CC involves contacting a CFTR nucleic acid from a subject with a primer set
 CC chosen from any one of 553 fully defined 15-100 nt sequences given in
 CC specification, generating an extension product from the primer set having
 CC a mutation or polymorphism, and analyzing the extension product. The
 CC invention further comprises: a method for identifying the presence or
 CC absence of a genetic marker in the cystic fibrosis transmembrane
 CC conductance regulator (CFTR) gene of a subject, which involves providing
 CC a DNA sample from the subject, providing at least one primer set that is
 CC any number between 1-75 nucleotides upstream or downstream of a primer
 CC set described in the specification, contacting the DNA and at least one
 CC primer set, generating an extension product that comprises a region of
 CC DNA that includes the location of the genetic marker, separating the
 CC extension product on a gel, and identifying the presence or absence of
 CC the genetic marker in the subject by analyzing the separation of the
 CC extension product; and the use of at least one primer set described in
 CC the specification to identify the presence or absence of a mutation or
 CC polymorphism on a CFTR gene. The method and primer sets are useful for
 CC identifying the presence or absence of a mutation or polymorphism in the
 CC cystic fibrosis transmembrane conductance regulator gene of a subject.
 CC This polynucleotide sequence represents a primer used in the CFTR gene
 CC mutation/polymorphism detection of the invention.
 XX
 SQ Sequence 23 BP; 6 A; 1 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 67.4%; Score 12.8; DB 14; Length 23;
 Best Local Similarity 87.5%; Pred. No. 5.9e+04;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GGAGAAGGGGTGGGTG 16
 |||||
 DB 8 GGAGAAGGGGTGGGTG 23

RESULT 35
 AAV15574/C
 ID AAV15574 standard; DNA; 24 BP.
 XX AC
 XX AAV15574;
 XX DT
 XX 22-MAY-1998 (first entry)
 XX DE
 XX Primer for HIV RNA.
 XX KW Human immunodeficiency virus; HIV; inhibition; replication;
 XX KW human topoisomerase I; human topo I; treatment; prevention; PCR primer;
 XX KW ss.
 XX OS Synthetic.
 XX OS Human immunodeficiency virus.
 XX PN
 XX WO9744492-A1.
 XX PD
 XX 27-NOV-1997.
 XX PF
 XX 22-MAY-1997; 97WO-US008686.
 XX PR
 XX 23-MAY-1996; 96US-00652074.
 XX XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX PI
 XX Hall MW, Takahashi H;
 XX XX
 XX WPI; 1998-018542/02.
 XX DR
 XX Inhibiting replication of HIV in cells with topoisomerase I inhibitor -
 XX PT particularly camptothecin derivative, specifically used with other anti-
 XX PT HIV agents, also transgenic mice expressing topoisomerase for drug
 XX PT screening.
 XX XX
 XX Example 7; Page 51; 83pp; English.
 XX PS
 XX The present sequence was used in the development of a novel method for
 XX CC the inhibition of human immunodeficiency virus (HIV) replication in a

CC cell. The method comprises treating the cell with an agent that
CC interferes with interaction between human topoisomerase I (topo I) and
CC HIV proteins in the cell, useful in the treatment and prevention of HIV
CC infection

XX Sequence 24 BP; 2 A; 13 C; 2 G; 7 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 2; Length 24;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGT 16
||||| ||||| |||||
Db 16 GGAGGAGGAGTGGGT 1

RESULT 36
ABK51637
ID ABK51637 standard; DNA; 26 BP.
XX
AC ABK51637;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human ABCG5 gene splice junction sequence #7.
XX
KW Human; ABCG5; ATP-binding cassette gene 5; sitosterolemia; cholesterol;
KW arteriosclerosis; heart disease; hypersterolemia; Alzheimer's disease;
KW splice junction; ss.
XX
OS Homo sapiens.
XX
FN WO200227016-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US029859.
XX
PR 25-SEP-2000; 2000US-0235268P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (PATE/) PATEL S B.
PA (DEAN/) DEAN M.
PI Patel SB, Dean M;
XX
DR WPI; 2002-416483/44.
XX
PT Novel mammalian ATP-binding cassette gene 5 polypeptide, and the nucleic
PT acid encoding the polypeptide, useful for treating sitosterolemia,
PT arteriosclerosis and heart diseases.
XX
PS Example 1; Page 28; 66pp; English.

CC The present invention relates to a new mammalian ATP-binding cassette
CC gene 5 (ABCG5) polypeptide. The invention is useful for identifying a
CC predisposition for developing sitosterolemia, arteriosclerosis or heart
CC disease. The molecules of the invention are also useful for identifying a
CC compound which alters ABCG5 activity level comprising contacting a cell
CC culture or mammal which have ABCG5 polypeptide with a compound and
CC measuring ABCG5 biological activity in the cell culture or in mammal,
CC where an increase or decrease in ABCG5 biological activity compared to
CC ABCG5 biological activity in a control cell culture or mammal not
CC contacted with the compound, identifies a compound that increases or
CC decreases ABCG5 activity respectively. The cell culture or mammal
CC comprises a mutated ABCG5 polypeptide or a wild type polypeptide. The
CC ABCG5 biological activity, or level of ABCG5 mRNA, or level of the
CC polypeptide in a cell culture or mammal is also compared with that of a
CC second cell culture or mammal comprising a wild type ABCG5 polypeptide.
CC Stimulation of ABCG5 activity is useful for treating or preventing
CC hypersterolemia, arteriosclerosis, heart disease and/or Alzheimer's
CC disease. The method of the invention is useful for increasing cholesterol
CC excretion and/or decreasing cholesterol adsorption. The present nucleic

CC acid sequence represents one of a collection (ABK51631-ABK51654) of human
CC ABCG5 gene splice junction sequences

XX Sequence 26 BP; 6 A; 9 C; 9 G; 2 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 6; Length 26;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGC 18
||||| ||||| |||||
Db 3 AGAAGGAGGTGGGTGC 18

RESULT 37
ADZ15700
ID ADZ15700 standard; DNA; 26 BP.
XX
AC ADZ15700;
XX
DT 16-JUN-2005 (first entry)
XX
DE Mutagenic PCR primer used to amplify human p53 cDNA - SEQ ID 510.
XX
KW DNA library; DNA microarray; mutagenesis; PCR; primer; ss; p53 gene.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN JP2003265187-A.
XX
PD 24-SEP-2003.
XX
PF 19-MAR-2002; 2002JP-00076990.
XX
PR 19-MAR-2002; 2002JP-00076990.
XX
PA (TOHO-) TOHOKU TECHNOARCH KK.
XX
DR WPI; 2004-183645/18.
XX
PT Constructing a mutant p53 gene library by performing first PCR using
PT oligonucleotide specifying mutation induction as primer, performing
PT second PCR using product of first PCR, as megaprimer and PCR cloning a
PT PCR product in gap repair vector.
XX
PS Claim 8; SEQ ID NO 512; 664pp; Japanese.

CC The invention relates to a novel method for constructing a comprehensive
CC p53 mutant gene library. The method comprises carrying out a first PCR
CC using an oligonucleotide specifying mutation induction as a primer, and
CC then carrying out a second PCR using the PCR product obtained from first
CC PCR as a megaprimer, and cloning the PCR product thus obtained into a gap
CC repair vector. The method of the invention may be useful for constructing
CC a comprehensive p53 mutant gene library. The mutant gene library thus
CC obtained, is useful for preparing nucleic acid arrays and analyzing the
CC p53 gene. The current sequence is that of a mutagenic PCR primer of the
CC invention which was used to amplify, and thus introduce a single mutation
CC into, a human p53 cDNA.

XX Sequence 26 BP; 3 A; 4 C; 16 G; 3 T; 0 U; 0 Other;
SQ

Query Match 67.4%; Score 12.8; DB 13; Length 26;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTGC 18
||||| ||||| |||||
Db 5 AGGAGGGGGTGGGTGC 20

RESULT 38
AAX14972/c

```

ID AAX14972 standard; DNA; 27 BP.
XX AC
XX AAX14972;
XX DT
XX 24-MAR-1999 (first entry)
XX DE Triple helix forming nucleotides 1427-1453 of the p53 gene.
XX KW Triple-helix forming region; Triplex formation; DNA detection;
XX KW identification; bacteria; oncogene; virus; ds.
XX OS Homo sapiens.
XX PN US5861244-A.
XX PD 19-JAN-1999.
XX PF 22-DEC-1993; 93US-00173489.
XX PR 29-OCT-1992; 92US-00968436.
XX PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX PI Hepburn AG, Wang C;
XX WPI; 1999-130384/11.
XX DT
XX Assay of genetic sequences based on triplex formation from double
XX PT stranded analyte - and hybrid of anchor and reporter sequences, with
XX PT reporter released if triplex formation occurs, used e.g. to identify
XX PT bacteria.
XX PS Disclosure; Col 25-26; 168pp; English.
XX CC The present sequence represents a potential triple-helix forming region.
XX CC It can be used to demonstrate the assay of the invention. The assay
XX CC comprises adding a sample containing double-stranded DNA test sequences,
XX CC e.g. containing the present sequence, to an aqueous medium containing at
XX CC least one complex of anchor DNA, attached to a solid support, and
XX CC reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX CC designed to form a triple-strand structure with part of the test
XX CC sequence. Triplex formation results in displacement of the reporter DNA
XX CC which is detected as an indication of the presence of the DNA test
XX CC sequence. The method is used to detect DNA sequences, particularly for
XX CC identification of bacteria (by detecting genes for ribosomal RNA) in
XX CC clinical samples, but also detection of oncogenes and Hepatitis B virus
XX CC
XX SQ Sequence 27 BP; 2 A; 19 C; 0 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 67.4%; Score 12.8; DB 2; Length 27;
XX Best Local Similarity 87.5%; Pred. No. 5.8e+04;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 2 GAGAGGGGGTGGGTG 17
DB 17 GAGATGGGGTGGGTG 2
    ||||| ||||| |||||
RESULT 39
ADXS58930/c
ID ADXS58930 standard; DNA; 29 BP.
XX AC
XX ADXS58930;
XX DT
XX 05-MAY-2005 (first entry)
XX DE Mouse DG239 TaqMan probe.
XX KW Pancreas disease; metabolic disorder; obesity; syndrome x; analgesic;
XX KW anti-anigal; insulin dependent diabetes mellitus;
XX KW non-insulin dependent diabetes; antidiabetic; anorectic; cytostatic;
XX KW anti-inflammatory; gene therapy; diagnosis; antisense therapy; DG239;
XX KW probe; ss.
XX
XX OS Mus sp.
XX Key Location/Qualifiers
XX modified_base 1 /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 5' FAM label"
XX modified_base 29
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "OTHER= 3' TAMRA label"
XX
XX WO2005014029-A2.
XX PN
XX PD 17-FEB-2005.
XX PF 15-JUL-2004; 2004WO-EP007916.
XX PR 16-JUL-2003; 2003EP-00016171.
XX PR 17-JUL-2003; 2003EP-00016246.
XX PR 22-JUL-2003; 2003EP-00016711.
XX PR 12-AUG-2003; 2003EP-00018326.
XX
XX (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX PI Onichtchouk D;
XX
XX WPI; 2005-152508/16.
XX
XX New pharmaceutical composition having a DG008, DG065, DG210 or DG239
XX PT protein and/or encoding nucleic acid molecule, useful for diagnosing,
XX PT preventing or treating pancreatic diseases, such as diabetes, obesity and
XX PT metabolic syndrome.
XX
XX Example 3; SEQ ID NO 20; 82pp; English.
XX
XX The invention relates to secreted factors referred to as DG008, DG065,
XX DG210 and DG239 ADXS58911-ADXS58918, which are involved in pancreas
XX development, regeneration, and in the regulation of energy homeostasis.
XX These were identified in a screen for secreted factors expressed in
XX developing mammalian (mouse) pancreas. A claimed pharmaceutical
XX composition comprises a DG008, DG065, DG210 or DG239 protein (or
XX functional fragment), a nucleic acid molecule encoding the protein (or
XX functional fragment), and/or an effector/modulator of the protein or
XX nucleic acid. The composition can be used in the manufacture of an agent
XX for detection and/or verifying, for the treatment, alleviation and/or
XX prevention of pancreatic diseases (e.g. diabetes such as insulin
XX dependent diabetes mellitus or non-insulin dependent diabetes mellitus),
XX obesity, metabolic syndrome (syndrome x) and/or other metabolic diseases
XX or dysfunctions. It can also be used for the manufacture of an agent for
XX the modulation of pancreatic development or for the regeneration of
XX pancreatic tissues or cells, particularly pancreatic beta cells, and may
XX be used in vivo or in vitro. The invention also provides a non-human
XX transgenic animal in which expression of DG008, DG065, DG210 or DG239 is
XX increased or reduced, recombinant host cells, a method of identifying a
XX (poly)peptide involved in the regulation of energy homeostasis, and a
XX method of screening for an agent the effects/modulates the activity of
XX DG008, DG065, DG210 or DG239 or its interaction with a binding target.
XX The present sequence is that of a Taqman probe for mouse DG239. This was
XX used in an example from the invention in a quantitative analysis of
XX expression of DG239 nucleic acids in different mouse tissues.
XX
XX Sequence 29 BP; 10 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 67.4%; Score 12.8; DB 14; Length 29;
XX Best Local Similarity 87.5%; Pred. No. 5.8e+04;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 3 AGAAGGGGGTGGGTGC 18
DB 20 AGTAGGGGTGGGTGC 5
    ||||| ||||| |||||

```

RESULT 40
ID ADW28628 standard; DNA; 30 BP.
XX
AC ADW28628;
XX
DT 07-APR-2005 (first entry)
XX
DE HER-2 splice isoform 1 peptide oligonucleotide, SEQ ID 5.
XX
KW Cytostatic; Antirheumatic; Antidiabetic; Cardiant; Nootropic;
KW Neuroprotective; antibody identification; antibody production;
KW antibody therapy; cancer; ss.
XX
OS Homo sapiens.
XX
PN US2005009110-A1.
XX
PD 13-JAN-2005.
XX
PF 08-JUL-2003; 2003US-00615343.
XX
PR 08-JUL-2003; 2003US-00615343.
XX
PA (CHAN/) CHANG X.
XX
PI Chang X;
XX
DR WPI; 2005-099971/11.
XX
DR P-PSDB; ADW28629.
XX
PT Identifying antibody to protein, involves contacting solid surface coated
PT with antibodies with fusion protein having portion of target protein and
PT carrier protein and conducting assay to determine presence of carrier
PT protein.
XX
PS Example 4; SEQ ID NO 5; 55pp; English.
XX
CC The present invention relates to a method for identifying antibodies for
CC target proteins. The method comprises: (i) contacting an antibody-coated
CC solid surface with a fusion protein, where the antibodies bind
CC specifically to the fusion protein and the fusion protein comprises at
CC least a portion of the target protein linked to a carrier protein, and
CC (ii) conducting an assay to determine the presence of the carrier
CC protein, where the presence of a carrier protein indicates the presence
CC of an antibody to the target protein. The target protein may be an
CC isoform of a protein that is associated with disease, e.g. Vascular
CC Endothelial Growth Factor (VEGF) isoforms VEGF165 (ADW28644) and VEGF121
CC (PSN; ADW28645), which are associated with cancer; Prostate Specific Antigen
CC (PSA; ADW28642), which is associated with prostate cancer and Her2
CC (ADW28640), which is associated with breast cancer. Also claimed are
CC methods for: generating (M2) monoclonal antibodies, where each monoclonal
CC antibody binds to a target protein, specifically at least one monoclonal
CC antibody that binds to an isoform of a protein that is associated with a
CC disease; isolating (M3) an antibody binding specifically to a target
CC protein from several antibodies that are associated with the nucleic
CC acid(s) encoding the antibody; determining (M4) the presence of an
CC antigen in a sample; and identifying (M5) an epitope on a target protein.
CC The antibodies identified by (M1) are useful for treating or preventing
CC diseases in which the presence of an antibody to a particular molecule is
CC beneficial. The antibodies are useful for targeting agents such as toxins
CC to particular cells e.g., cancer cell. (M1) is useful for identifying
CC epitopes on target protein which are used for preparing DNA vaccines
CC having nucleotide sequences encoding epitope of a disease associated
CC protein isoforms used for prevention or treatment of diseases such as
CC cancer, rheumatoid arthritis, diabetes, acute myeloid leukemia (AML),
CC chronic lymphocytic leukemia (CLL), ovarian cancer, prostate cancer,
CC cardiovascular disease, Alzheimer's disease, etc. The antibodies are
CC useful for detecting antigens e.g. in specific cells, tissue or bodily
CC fluids such as serum, or for affinity purification of antigen from
CC recombinant cell culture or natural sources. The present sequence is an
CC oligonucleotide encoding a HER-2 isoform epitope, which can be used to

CC produce a HER-2 isoform fusion protein.
XX
SQ Sequence 30 BP; 6 A; 15 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 67.4%; Score 12.8; DB 14; Length 30;
Best Local Similarity 87.5%; Pred. No. 5.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AGAAGGGGGTGGGTGC 18
Db 23 AGAGGGGAGTGGGTGC 8
RESULT 41
ID ADF93340 standard; RNA; 19 BP.
XX
AC ADF93340;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human TERT transcript target sequence/siNA upper strand, SEQ ID 57.
XX
KW Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
KW neuroprotective; anti-HIV; ophthalmological; antiulcer; antirheumatic;
KW antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
KW RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
XX
OS Homo sapiens.
XX
PN WO2003070742-A1.
XX
PD 28-AUG-2003.
XX
PF 11-FEB-2003; 2003WO-US004088.
XX
PR 20-FEB-2002; 2002US-0358580P.
XX
PR 11-MAR-2002; 2002US-0363124P.
XX
PR 06-JUN-2002; 2002US-0386782P.
XX
PR 17-JUL-2002; 2002US-0396600P.
XX
PR 29-AUG-2002; 2002US-0406784P.
XX
PR 05-SEP-2002; 2002US-0408378P.
XX
PR 09-SEP-2002; 2002US-0409233P.
XX
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Beigelman L;
XX
DR WPI; 2003-689777/65.
XX
PT New short interfering nucleic acid downregulates expression of the
PT telomerase gene useful e.g. for treatment and diagnosis of cancer.
XX
PS Example 3; SEQ ID NO 57; 145pp; English.
XX
CC The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the one or more telomerase genes by RNA
CC interference. The siNAs may or may not comprise ribonucleotides and may
CC be double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
CC can contain deoxyribonucleotides, and can be chemically synthesised,
CC expressed from a vector or enzymatically synthesised. The invention also
CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
CC used to modulate expression of the telomerase genes in cells, tissue

CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
 CC transplants for the treatment of a variety of conditions. They may be
 CC used for treating cancer, restenosis, infectious diseases (specifically
 CC protozoal), transplant rejection, or autoimmune or age-related diseases,
 CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
 CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the upper strand of a human TERT-targeted double-stranded
 CC siNA, which is identical to the c-fos transcript target sequence.
 XX
 XX Sequence 19 BP; 1 A; 3 C; 13 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 66.3%; Score 12.6; DB 10; Length 19;
 Best Local Similarity 68.4%; Pred. No. 7.1e+04;
 Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGTGCT 19
 DB 1 GGAGCGGGCGGUGGGGCT 19
 RESULT 42
 ADF93594/c
 ID ADF93594 standard; RNA; 19 BP.
 XX
 AC ADF93594;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human TERT siNA lower strand, SEQ ID 321.
 XX
 KW Cytostatic; vasotropic; protozoacide; immunosuppressive; dermatological;
 KW neuroprotective; anti-HIV; ophthalmological; antiulcer; antirheumatic;
 KW antiarthritic; antiinflammatory; gene therapy; telomerase; human; terc;
 KW RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; TERC; TERT; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003070742-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 11-FEB-2003; 2003WO-US004088.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 17-JUL-2002; 2002US-0396600P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Beigelman L;
 XX
 DR WPI; 2003-689777/65.
 XX
 PT New short interfering nucleic acid downregulates expression of the
 PT telomerase gene useful e.g. for treatment and diagnosis of cancer.
 XX
 PS Example 3; SEQ ID NO 321; 145pp; English.
 XX
 CC The invention relates to short interfering nucleic acids (siNA) which
 CC downregulate expression of the one or more telomerase genes by RNA
 CC interference. The siNAs may or may not comprise ribonucleotides and may

CC be double or single stranded. They further comprise sense and antisense
 CC regions, or alternatively are assembled from a sense oligonucleotide and
 CC an antisense oligonucleotide. Specifically, the siNAs include short
 CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
 CC hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified,
 CC can contain deoxyribonucleotides, and can be chemically synthesised,
 CC expressed from a vector or enzymatically synthesised. The invention also
 CC relates to kits for the in vitro or in vivo delivery of siNA; conjugates
 CC and/or complexes of siNA; and vectors that express siNA. The siNAs are
 CC used to modulate expression of the telomerase genes in cells, tissue
 CC explants or organisms (e.g., by ex vivo gene therapy), or in grafts and
 CC transplants for the treatment of a variety of conditions. They may be
 CC used for treating cancer, restenosis, infectious diseases (specifically
 CC protozoal), transplant rejection, or autoimmune or age-related diseases,
 CC e.g. multiple sclerosis, lupus erythematosus, AIDS, macular degeneration,
 CC skin ulcers and rheumatoid arthritis. The siNAs are also useful for drug
 CC screening, diagnosis, therapeutic target identification and validation,
 CC genetic engineering, pharmacogenomics, studying gene function, and gene
 CC mapping (e.g., of single nucleotide polymorphisms). The present sequence
 CC represents the lower strand of a human TERT-targeted double-stranded
 CC siNA.
 XX
 XX Sequence 19 BP; 2 A; 13 C; 3 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 66.3%; Score 12.6; DB 10; Length 19;
 Best Local Similarity 78.9%; Pred. No. 7.1e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GGAGAGGGGGTGGTGCT 19
 DB 19 GGAGCGGGCGTGGGGCT 1
 RESULT 43
 ADG64570
 ID ADG64570 standard; RNA; 19 BP.
 XX
 AC ADG64570;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human G72 siNA oligonucleotide SEQ ID NO:16.
 XX
 KW RNA interference; short interfering nucleic acid; siNA;
 KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
 KW short hairpin RNA; shRNA; expression modulation; gene therapy;
 KW drug screening; diagnosis; therapeutic target identification;
 KW pharmacogenomics; gene function analysis; gene mapping; neuroleptic;
 KW schizophrenia; human; G72; target sequence; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070743-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-US004397.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 05-DEC-2002; 2002US-0431105P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Beigelman L, Haerberli P;
 XX
 DR WPI; 2003-712607/67.

XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of schizophrenia, downregulates expression of the G72 gene.
XX
XX Example 3; SEQ ID NO 16; 139pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human G72 gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the G72 gene in cells, tissue explants or organisms (e.g.,
CC by ex vivo gene therapy), or in grafts and transplants for the treatment
CC of a variety of conditions. The human G72 siNAs have neuroleptic activity
CC and can be used for treating schizophrenia. The siNAs are also useful for
CC drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the upper strand of a human G72-targeted
CC double-stranded siNA, which is identical to the G72 transcript target
CC sequence.
XX
XX Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;
SQ
Query Match 66.3%; Score 12.6; DB 10; Length 19;
Best Local Similarity 63.2%; Pred. No. 7.1e+04;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGGGTGCT 19
Db 1 GGAAAGCUGAGGUGCU 19
RESULT 44
ADG64626/c
ID ADG64626 standard; RNA; 19 BP.
XX
AC ADG64626;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human G72 siNA oligonucleotide SEQ ID NO:72.
XX
XX RNA interference; short interfering nucleic acid; siNA;
KW short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA;
KW short hairpin RNA; shRNA; expression modulation; gene therapy;
KW drug screening; diagnosis; therapeutic target identification;
KW pharmacogenomics; gene function analysis; gene mapping; neuroleptic;
KW schizophrenia; human; G72; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070743-A1.
XX
XX 28-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-US004397.
XX
XX 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0385782P.
PR 29-AUG-2002; 2002US-0408784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 05-DEC-2002; 2002US-0431105P.

PR 15-JAN-2003; 2003US-0440129P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Meswiggen J, Beigelman L, Haeberli P;
XX WPI; 2003-712607/67.
XX
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of schizophrenia, downregulates expression of the G72 gene.
XX
XX Example 3; SEQ ID NO 72; 139pp; English.
XX
XX The invention relates to short interfering nucleic acids (siNA) which
CC downregulate expression of the human G72 gene by RNA interference. The
CC siNAs may or may not comprise ribonucleotides and may be double or single
CC stranded. They further comprise sense and antisense regions, or
CC alternatively are assembled from a sense oligonucleotide and an antisense
CC oligonucleotide. Specifically, the siNAs include short interfering RNA
CC (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA
CC (shRNA). The siNAs can be unmodified or chemically modified, can contain
CC deoxyribonucleotides, and can be chemically synthesised, expressed from a
CC vector or enzymatically synthesised. The invention also relates to kits
CC for the in vitro or in vivo delivery of siNA; conjugates and/or complexes
CC of siNA; and vectors that express siNA. The siNAs are used to modulate
CC expression of the G72 gene in cells, tissue explants or organisms (e.g.,
CC by ex vivo gene therapy), or in grafts and transplants for the treatment
CC of a variety of conditions. The human G72 siNAs have neuroleptic activity
CC and can be used for treating schizophrenia. The siNAs are also useful for
CC drug screening, diagnosis, therapeutic target identification and
CC validation, genetic engineering, pharmacogenomics, studying gene
CC function, and gene mapping (e.g., of single nucleotide polymorphisms).
CC The present sequence represents the lower strand of a human G72-targeted
CC double-stranded siNA.
XX
XX Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
SQ
Query Match 65.3%; Score 12.6; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGAGAAGGGGGTGGGTGCT 19
Db 19 GGAAAGCTGATGGGTGCT 1
RESULT 45
AEB17755/c
ID AEB17755 standard; RNA; 19 BP.
XX
XX AEB17755;
XX
XX 25-AUG-2005 (first entry)
XX
XX G72 siRNA molecule complement sequence/target oligo, SEQ ID 72.
XX
XX short interfering RNA; siRNA; G72; RNA interference; gene silencing;
KW neuroleptic; antisense therapy; Amino acid oxidase; schizophrenia; ss.
XX
XX Synthetic.
OS
XX US2005136436-A1.
XX
XX 23-JUN-2005.
XX
XX 19-AUG-2004; 2004US-00923640.
XX
XX 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.

PR 20-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 05-DEC-2002; 2002US-0431105P.
PR 15-JAN-2003; 2003US-0440129P.
PR 13-FEB-2003; 2003WO-US004397.
PR 20-FEB-2003; 2003WO-US005028.
PR 20-FEB-2003; 2003WO-US005346.
PR 30-APR-2003; 2003US-00427160.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-0543480P.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Haerberli P;
XX WPI; 2005-466131/47.
XX
XX New chemically synthesized double stranded short interfering nucleic acid
PT (siNA) molecule directing cleavage of a G72 RNA via RNA interference
PT (RNAi), useful in diagnosing or treating schizophrenia.
XX
XX Claim 33; SEQ ID NO 72; 127pp; English.
XX
XX The invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid (siNA) molecule that directs cleavage of a
CC G72 RNA via RNA interference (RNAi). Each strand of the siNA molecule is
CC 18-23 nucleotides in length, and one strand of the siNA molecule
CC comprises a nucleotide sequence having sufficient complementarity to the
CC G72 RNA for the siNA molecule to direct cleavage of the G72 RNA via RNA
CC interference. The invention also includes a composition comprising the
CC siNA cited above in a pharmaceutical carrier or diluent. The siNA oligos
CC have neuroleptic activity and are useful in antisense therapy. The
CC methods and compositions of the present invention are useful for
CC modulating G72 and/or D-amino acid oxidase (DAAO) gene expression using
CC short interfering nucleic acid molecules, in particular for diagnosing or
CC treating conditions that respond to modulation of G72 and/or DAAO
CC expression or activity, such as schizophrenia. This oligo sequence
CC represents a G72 cleavage directing siNA molecule complement
CC sequence/target of the invention.
XX
XX Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
SQ
Query Match 66.3%; Score 12.6; DB 14; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGTGCT 19
DB 19 GGAAAGCTGATGGTGCT 1
RESULT 46
AEB17699
ID AEB17699 standard; RNA; 19 BP.
AC AEB17699;
XX
XX 25-AUG-2005 (first entry)
DT
XX
XX G72 siRNA molecule complement sequence/target oligo, SEQ ID 16.
DE
XX short interfering RNA; siRNA; G72; RNA interference; gene silencing;
KW

KW neuroleptic; antisense therapy; Amino acid oxidase; schizophrenia; ss.
XX Synthetic.
XX US2005136436-A1.
XX
XX 23-JUN-2005.
XX
XX 19-AUG-2004; 2004US-00923640.
XX
XX 18-MAY-2001; 2001US-0292217P.
XX 20-JUL-2001; 2001US-0306883P.
XX 13-AUG-2001; 2001US-0311865P.
XX 20-FEB-2002; 2002US-0358580P.
XX 06-MAR-2002; 2002US-0362016P.
XX 11-MAR-2002; 2002US-0363124P.
XX 20-MAY-2002; 2002WO-US015876.
XX 06-JUN-2002; 2002US-0386782P.
XX 29-AUG-2002; 2002US-0406784P.
XX 05-SEP-2002; 2002US-0408378P.
XX 09-SEP-2002; 2002US-0409293P.
XX 05-DEC-2002; 2002US-0431105P.
XX 15-JAN-2003; 2003US-0440129P.
XX 13-FEB-2003; 2003WO-US004397.
XX 20-FEB-2003; 2003WO-US005028.
XX 20-FEB-2003; 2003WO-US005346.
XX 30-APR-2003; 2003US-00427160.
XX 23-MAY-2003; 2003US-00444853.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 03-DEC-2003; 2003US-00727780.
XX 14-JAN-2004; 2004US-00757803.
XX 10-FEB-2004; 2004US-0543480P.
XX 13-FEB-2004; 2004US-00780447.
XX 16-APR-2004; 2004US-00826966.
XX 30-APR-2004; 2004WO-US013456.
XX 24-MAY-2004; 2004WO-US016390.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Haerberli P;
XX WPI; 2005-466131/47.
XX
XX New chemically synthesized double stranded short interfering nucleic acid
PT (siNA) molecule directing cleavage of a G72 RNA via RNA interference
PT (RNAi), useful in diagnosing or treating schizophrenia.
XX
XX Claim 33; SEQ ID NO 72; 127pp; English.
XX
XX The invention relates to a novel chemically synthesized double stranded
CC short interfering nucleic acid (siNA) molecule that directs cleavage of a
CC G72 RNA via RNA interference (RNAi). Each strand of the siNA molecule is
CC 18-23 nucleotides in length, and one strand of the siNA molecule
CC comprises a nucleotide sequence having sufficient complementarity to the
CC G72 RNA for the siNA molecule to direct cleavage of the G72 RNA via RNA
CC interference. The invention also includes a composition comprising the
CC siNA cited above in a pharmaceutical carrier or diluent. The siNA oligos
CC have neuroleptic activity and are useful in antisense therapy. The
CC methods and compositions of the present invention are useful for
CC modulating G72 and/or D-amino acid oxidase (DAAO) gene expression using
CC short interfering nucleic acid molecules, in particular for diagnosing or
CC treating conditions that respond to modulation of G72 and/or DAAO
CC expression or activity, such as schizophrenia. This oligo sequence
CC represents a G72 cleavage directing siNA molecule complement
CC sequence/target of the invention.
XX
XX Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
SQ
Query Match 66.3%; Score 12.6; DB 14; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGTGCT 19
DB 19 GGAAAGCTGATGGTGCT 1
RESULT 46
AEB17699
ID AEB17699 standard; RNA; 19 BP.
AC AEB17699;
XX
XX 25-AUG-2005 (first entry)
DT
XX
XX G72 siRNA molecule complement sequence/target oligo, SEQ ID 16.
DE
XX short interfering RNA; siRNA; G72; RNA interference; gene silencing;
KW

```
Qy 1 GGAGAGGGGGTGGTGCT 19
Db 1 GGAAAGCUGAUGGUGUCU 19

RESULT 47
AEB15820/c
ID AEB15820 standard; RNA; 19 BP.
AC AEB15820;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human telomerase-targeted siRNA strand SeqID311.
XX
KW RNA interference; gene silencing; short interfering RNA; siRNA;
KW cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
KW restenosis; transplant rejection; autoimmune disease; hyperproliferation;
KW aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
KW telomerase.
XX
OS Homo sapiens.
XX
PN US2005153916-A1.
XX
PD 14-JUL-2005.
XX
PF 20-AUG-2004; 2004US-00923330.
XX
PR 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 17-JUL-2002; 2002US-0396600P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 11-FEB-2003; 2003WO-US004088.
PR 20-FEB-2003; 2003WO-US005028.
PR 30-APR-2003; 2003US-0044853.
PR 23-MAY-2003; 2003US-00693059.
PR 24-OCT-2003; 2003US-00720448.
PR 23-NOV-2003; 2003US-00727780.
PR 03-DEC-2003; 2003US-00757803.
PR 14-JAN-2004; 2004US-0543480P.
PR 10-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L;
XX
XX WPI; 2005-496858/50.
XX
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of telomerase RNA by RNA interference,
PT useful for treating cancer and restenosis.
XX
XX Claim 33; SEQ ID NO 311; 304pp; English.
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
```

```
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising an siRNA targeted to the human telomerase mRNA
CC which may have a cytostatic, immunosuppressive, vasotropic or
CC antimicrobial activity. The invention further discloses expression
CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
CC used to modulate expression of the telomerase gene in cells, tissue
CC explants or organisms (for example by ex vivo gene therapy), or in grafts
CC and transplants for the treatment of a variety of conditions. They may be
CC used in the treatment of cancer, restenosis, transplant and/or tissue
CC rejection, and/or autoimmune, proliferative, infectious, and age-related
CC diseases, disorders or conditions. The siRNAs may also be used in drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (for example of single nucleotide polymorphisms). The present
CC sequence represents the antisense strand of a human telomerase-targeted
CC double-stranded siRNA.
XX
SQ Sequence 19 BP; 2 A; 13 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 66.3%; Score 12.6; DB 14; Length 19;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGTGCT 19
Db 19 GGAGCGGGCGTGGGGCT 1

RESULT 48
AEB15597
ID AEB15597 standard; RNA; 19 BP.
AC AEB15597;
XX
XX 22-SEP-2005 (first entry)
XX
DE Human telomerase-targeted siRNA strand SeqID88.
XX
KW RNA interference; gene silencing; short interfering RNA; siRNA;
KW cytosolic; immunosuppressive; vasotropic; antimicrobial; cancer;
KW restenosis; transplant rejection; autoimmune disease; hyperproliferation;
KW aging; drug screening; diagnostic; genetic engineering; gene mapping; ss;
KW telomerase.
XX
OS Homo sapiens.
XX
XX US2005153916-A1.
XX
PD 14-JUL-2005.
XX
PF 20-AUG-2004; 2004US-00923330.
XX
PR 18-MAY-2001; 2001US-0292217P.
PR 20-JUL-2001; 2001US-0306883P.
PR 13-AUG-2001; 2001US-0311865P.
PR 20-FEB-2002; 2002US-0358580P.
PR 06-MAR-2002; 2002US-0362016P.
PR 11-MAR-2002; 2002US-0363124P.
PR 20-MAY-2002; 2002WO-US015876.
PR 06-JUN-2002; 2002US-0386782P.
PR 17-JUL-2002; 2002US-0396600P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
PR 11-FEB-2003; 2003WO-US004088.
PR 20-FEB-2003; 2003WO-US005028.
PR 30-APR-2003; 2003US-0044853.
PR 23-MAY-2003; 2003US-00693059.
PR 24-OCT-2003; 2003US-00720448.
PR 23-NOV-2003; 2003US-00727780.
PR 03-DEC-2003; 2003US-00757803.
PR 14-JAN-2004; 2004US-0543480P.
PR 10-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004WO-US013456.
PR 24-MAY-2004; 2004WO-US016390.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L;
XX
XX WPI; 2005-496858/50.
XX
XX Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of telomerase RNA by RNA interference,
PT useful for treating cancer and restenosis.
XX
XX Claim 33; SEQ ID NO 311; 304pp; English.
XX
XX The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
```

PR 23-MAY-2003; 2003US-00444853.
PR 23-OCT-2003; 2003US-00693059.
PR 24-NOV-2003; 2003US-00720448.
PR 03-DEC-2003; 2003US-00727780.
PR 14-JAN-2004; 2004US-00757803.
PR 10-FEB-2004; 2004US-05434808.
PR 13-FEB-2004; 2004US-00780447.
PR 16-APR-2004; 2004US-00826966.
PR 30-APR-2004; 2004US-0013456.
PR 24-MAY-2004; 2004WO-US016390.
PA (SIRN-) SIENA THERAPEUTICS INC.
XX
XX
PI Mcswiggen J, Beigelman L;
XX
DR WPI; 2005-496858/50.
XX
PT Novel chemically synthesized double-stranded short interfering nucleic
PT acid molecule directing cleavage of telomerase RNA by RNA interference,
PT useful for treating cancer and restenosis.
XX
XX
PS Claim 33; SEQ ID NO 88; 304pp; English.
XX
CC The invention relates to chemically synthesized short interfering nucleic
CC acids (siRNAs) which downregulate expression of telomerase genes by RNA
CC interference. The siRNAs may or may not comprise ribonucleotides, can
CC contain deoxyribonucleotides, can be chemically modified and may be
CC double or single stranded. They further comprise sense and antisense
CC regions, or alternatively are assembled from a sense oligonucleotide and
CC an antisense oligonucleotide. Specifically, the siRNAs include short
CC interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short
CC hairpin RNA (shRNA). The invention also relates to pharmaceutical
CC compositions comprising a siRNA targeted to the human telomerase mRNA
CC which may have a cytostatic, immunosuppressive, vasotropic or
CC antimicrobial activity. The invention further discloses expression
CC vectors and host cells comprising an siRNA of the invention. The siRNAs are
CC used to modulate expression of the telomerase gene in cells, tissue
CC explants or organisms (for example by ex vivo gene therapy), or in grafts
CC and transplants for the treatment of a variety of conditions. They may be
CC used in the treatment of cancer, restenosis, transplant and/or tissue
CC rejection, and/or autoimmune, proliferative, infectious, and age-related
CC diseases, disorders or conditions. The siRNAs may also be used in drug
CC screening, diagnosis, therapeutic target identification and validation,
CC genetic engineering, pharmacogenomics, studying gene function, and gene
CC mapping (for example of single nucleotide polymorphisms). The present
CC sequence represents the sense strand of a human telomerase-targeted
CC double-stranded siRNA, which is identical to the telomerase transcript
CC target sequence.
XX
XX
SQ Sequence 19 BP; 1 A; 3 C; 13 G; 0 T; 2 U; 0 Other;
Query Match 66.3%; Score 12.6; DB 14; Length 19;
Best Local Similarity 68.4%; Pred. No. 7.1e+04;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGGAGGGGGTGGGTGCT 19
Db 1 GGAGCGGGCGGGGGGGCU 19
RESULT 49
AAC66150/c
ID AAC66150 standard; cDNA; 23 BP.
XX
XX AAC66150;
XX
XX
DT 13-FEB-2001 (first entry)
XX
DE 21-hydroxylase intron 2 cDNA fragment SEQ ID 14.
XX
XX
KW Congenital adrenal hyperplasia; diagnosis; 21-hydroxylase; exon 1;
KW intron 2; exon 4; HLA class III; human; ss.
XX

OS Synthetic.
XX
PN WO200063431-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-KR000347.
XX
PR 17-APR-1999; 99KR-00013671.
XX
PA (SMSU) SAMSUNG FINE CHEM CO LTD.
XX
XX Jin DK;
PI
DR WPI; 2000-679607/66.
XX
XX
PT Diagnosing congenital adrenal hyperplasia by attaching fragments of 21-
PT hydroxylase gene to substrates, amplifying DNA segments containing gene
PT copies from testis DNA, hybridizing gene and analyzing results.
XX
XX
PS Claim 6; Page 42; 46pp; English.
XX
CC This invention relates to a method for diagnosing congenital adrenal
CC hyperplasia. The method comprises attaching fragments of 21-hydroxylase
CC gene (exon 1, intron 2, exon 4) to substrates, amplifying DNA segments
CC containing copies of the gene from genomic DNA of testis using PCR,
CC hybridising the gene with the PCR product and analysing the results of
CC hybridisation. The steroid 21-hydroxylase gene is located in the HLA
CC class III gene region on chromosome 6. The method is used for the
CC diagnosis of congenital hyperplasia. Oligonucleotides AAC66148 - AAC66161
CC are fragments and antisense oligonucleotides of the 21-hydroxylase gene
CC (exon 1, intron 2, and exon 4). The 21-hydroxylase gene sequence is
CC represented in AAC66162, and PCR primers AAC66163 - AAC66172 are used to
CC amplify exon 1, intron 2, and exon 4 of the 21-hydroxylase gene in
CC examples illustrating the method of the invention
XX
XX
SQ Sequence 23 BP; 4 A; 12 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 66.3%; Score 12.6; DB 3; Length 23;
Best Local Similarity 78.9%; Pred. No. 7.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGAGGAGGGGGTGGGTGCT 19
Db 23 GCAGGAGGAGGTGGGGGCT 5
RESULT 50
AEF42944/c
ID AEF42944 standard; DNA; 23 BP.
XX
XX AEF42944;
XX
XX
DT 23-MAR-2006 (first entry)
XX
DE Human ABC gene, ABC10, reverse real time RT-PCR primer.
XX
XX ABC10; ABC transporter; multi-drug resistance; ss; RT-PCR;
KW reverse transcriptase PCR; primer; cancer; cytostatic; neoplasm;
KW drug discovery; ATP-binding cassette; pharmaceutical.
XX
XX Homo sapiens.
XX
XX WO2006009765-A2.
XX
XX 26-JAN-2006.
XX
XX 16-JUN-2005; 2005WO-US021253.
XX
XX 18-JUN-2004; 2004US-0580397P.
XX
XX 19-AUG-2004; 2004US-0602640P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Szakacs G, Annereau J, Lababidi S, Gottesman MM, Weinstein J;
 XX WPI; 2006-154816/16.
 XX
 XX Use of antiproliferative agent having therapeutic activity that is
 PT potentiated by ATP-binding cassette transporter protein for inhibiting
 PT growth of neoplastic cells during treatment of multi-drug resistance
 PT cancer.
 XX
 XX Example 1; SEQ ID NO 64; 99pp; English.
 PS
 PS
 XX The invention relates to inhibiting (M1) growth of neoplastic cells or
 CC development of multidrug resistance phenotype in cancer involving
 CC administration of an antiproliferative agent where the antiproliferative
 CC effect of the agent is potentiated by an ATP-binding cassette (ABC)
 CC transporter protein such as ABCB1 transporter. Also included are
 CC identification (M2) of therapeutic compounds having a therapeutic
 CC activity that is potentiated by the expression of an ATP-binding cassette
 CC (ABC) transporter gene (involving determining the expression level of at
 CC least one ABC gene in a panel of cell lines, determining the level of
 CC therapeutic activity of at least one test compound on the panel of cell
 CC lines and comparing the level of therapeutic activity with the expression
 CC level of the ABC gene, where a positive correlation between the level of
 CC therapeutic activity and the expression level of the ABC gene identifies
 CC the test compound as having an activity that is potentiated by the
 CC expression of the ABC gene) and identifying (M3) therapeutic compounds as
 CC substrates for ABC transporters (involving carrying out (M2), where a
 CC negative correlation between the level of therapeutic activity and the
 CC expression level of the ABC gene identifies the test compound as the
 CC substrate for the ABC transporter). The antiproliferative agent is
 CC hydrazine derivative of formulae given in the specification. The method
 CC is useful for inhibiting the development of multidrug resistance
 CC phenotype in cancer and for treatment of multi-drug resistant cancer
 CC (including colon carcinoma, renal carcinoma, hepatoma, adrenocortical
 CC carcinoma, pancreatic carcinoma, breast cancer, ovarian cancer, sarcoma,
 CC small cell lung cancer, acute myeloid leukemia, chronic myeloid leukemia,
 CC acute lymphoblastic leukemia, non-Hodgkin's lymphoma, B-cell lymphoma,
 CC and T-cell lymphoma). The present sequence is a real time RT-PCR primer
 CC for a Human ABC gene used to assay expression of the ABC gene in the
 CC method of the invention.
 XX
 XX Sequence 23 BP; 4 A; 11 C; 4 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 66.3%; Score 12.6; DB 15; Length 23;
 Best Local Similarity 78.9%; Fred. No. 7.1e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 1 GGAGAGGGGGTGGTGCT 19
 Db 23 GGTGAAGGGGGCCGAGCT 5
 Search completed: October 14, 2006, 19:40:52
 Job time : 353 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:38:30 ; Search time 2259 Seconds
(without alignments)
470.326 Million cell updates/sec

Title: US-10-604-926A-4539
Perfect score: 19
Sequence: 1 ggagaaggggtgggtgct 19
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 56556

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : EST:
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_hic.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.4	81.1	28	11	AZ393146
2	13.4	70.5	22	11	AZ307952
3	13.2	69.5	22	1	AI673793
4	12.8	67.4	25	1	AI586975
5	12.8	67.4	29	3	BQ590098
6	12.6	66.3	22	11	AZ479594
7	12.4	65.3	20	11	AZ345548
8	12.4	65.3	24	11	AZ486450
9	12.2	64.2	22	1	AI000026
10	12.2	64.2	22	11	AZ792883
11	12.2	64.2	23	11	AZ800080
12	12.2	64.2	25	11	AZ943422
13	12.2	64.2	26	11	AZ362697
14	12.2	64.2	27	11	AZ836891
15	12.2	64.2	28	1	AI785472
16	12.2	64.2	28	11	AZ483923
17	12.2	64.2	28	11	AZ774078
18	12.2	64.2	29	11	AZ642459
19	12.2	64.2	30	11	AZ361601

C 93	10.8	56.8	30	11	A2447206	1M0244J07	C 166	10.6	55.8	28	11	AZ640161	1M0501G23
C 94	10.6	55.8	19	11	A2447198	1M0244A10	C 167	10.6	55.8	28	11	AZ806290	2M0068C13
C 95	10.6	55.8	19	11	A2760597	1M0554N21	C 168	10.6	55.8	28	11	AZ872959	2M0186F03
C 96	10.6	55.8	19	11	A2962769	2M0231P08	C 169	10.6	55.8	28	12	CG734031	1119161H0
C 97	10.6	55.8	20	11	A2512326	1M0351I18	C 170	10.6	55.8	28	13	CW020469	CG0736 TI
C 98	10.6	55.8	20	11	A2645269	1M0510B10	C 171	10.6	55.8	28	14	DX072937	KBF0803C1
C 99	10.6	55.8	20	11	A2653361	1M0527D04	C 172	10.6	55.8	29	11	AZ387832	1M0147F23
C 100	10.6	55.8	20	11	A2653755	1M0537F22	C 173	10.6	55.8	29	11	AZ423751	1M0203B22
C 101	10.6	55.8	20	11	A2969440	2M0242O12	C 174	10.6	55.8	29	11	AZ662726	1M0542C01
C 102	10.6	55.8	21	11	A2345432	1M0080D07	C 175	10.6	55.8	29	11	AZ662737	1M0548006
C 103	10.6	55.8	21	11	A2476392	1M0295F12	C 176	10.6	55.8	29	11	AZ780387	2M0017N12
C 104	10.6	55.8	21	11	A2512534	1M0358B07	C 177	10.6	55.8	29	13	CZ194796	FSY10543-
C 105	10.6	55.8	21	11	A2583408	1M0378N23	C 178	10.6	55.8	29	14	DU832768	KBF0501N1
C 106	10.6	55.8	21	11	A2653464	1M0527G11	C 179	10.6	55.8	30	7	BE275232	601122051
C 107	10.6	55.8	21	11	A2774703	2M0004G14	C 180	10.6	55.8	30	9	DN988789	ZEBRA 2F
C 108	10.6	55.8	21	11	A2783943	2M0026F05	C 181	10.6	55.8	30	11	AZ337154	1M0067B11
C 109	10.6	55.8	21	11	A2871715	2M0184B13	C 182	10.6	55.8	30	11	AZ464926	1M0274J04
C 110	10.6	55.8	21	11	A2969578	2M0242G20	C 183	10.6	55.8	30	11	AZ468615	1M0281D22
C 111	10.6	55.8	21	11	A2978432	2M0254G15	C 184	10.6	55.8	30	11	AZ588957	1M0397B08
C 112	10.6	55.8	21	14	AG188438	Pan trol	C 185	10.6	55.8	30	11	AZ650045	1M0520E05
C 113	10.6	55.8	22	1	AI738599	wi3902.x	C 186	10.6	55.8	30	11	AZ783172	2M0024F08
C 114	10.6	55.8	22	1	AI748552	sb54f11.y	C 187	10.6	55.8	30	11	AZ833458	2M0115I02
C 115	10.6	55.8	22	11	A2327083	1M0050D17	C 188	10.6	55.8	30	11	AZ864315	2M0173P16
C 116	10.6	55.8	22	11	A2331988	1M0060B11	C 189	10.6	55.8	30	11	AZ976285	2M0251H09
C 117	10.6	55.8	22	11	A2607348	1M0429D18	C 190	10.6	55.8	30	14	DU834752	KBF0501S01
C 118	10.6	55.8	22	11	A2645874	1M0511C07	C 191	10.6	55.8	30	14	AL935924	ArabiDops
C 119	10.6	55.8	22	11	A2871408	2M0184E16	C 192	10.4	54.7	19	11	AZ485264	1M0312Q02
C 120	10.6	55.8	22	11	A2876923	2M0192D07	C 193	10.4	54.7	22	1	AI566419	tr95c08.x
C 121	10.6	55.8	22	11	A2967291	2M0238J09	C 194	10.4	54.7	22	1	AI631347	tz83c04.x
C 122	10.6	55.8	22	14	DU834523	KBF0501A10	C 195	10.4	54.7	22	11	AZ584417	1M0374N13
C 123	10.6	55.8	22	14	DX076174	KBF0807G0	C 196	10.4	54.7	22	11	AZ592243	1M0403F05
C 124	10.6	55.8	22	2	BG926069	HNC23-1-E	C 197	10.4	54.7	27	11	AZ439712	1M0230A06
C 125	10.6	55.8	23	5	CF302431	7LEAF--07	C 198	10.4	54.7	27	11	AZ456814	1M0282G02
C 126	10.6	55.8	23	11	A2353803	1M0092O14	C 199	10.4	54.7	28	1	AI037937	ox53a11.x
C 127	10.6	55.8	23	11	A2418429	1M0194F02	C 200	10.4	54.7	28	1	AI635783	wA07d11.x
C 128	10.6	55.8	23	11	A2581259	1M0369N11	C 201	10.4	54.7	29	11	AZ802638	2M0061C08
C 129	10.6	55.8	23	11	A2800632	2M0059B17	C 202	10.4	54.7	29	11	AG189105	Pan trol
C 130	10.6	55.8	23	11	A2968672	2M0241B09	C 203	10.4	54.7	29	14	BG925569	HNC5-1-E2
C 131	10.6	55.8	24	11	A2331608	1M0509H12	C 204	10.2	53.7	18	2	AG189105	HNC5-1-E2
C 132	10.6	55.8	24	11	A2346754	1M0082E12	C 205	10.2	53.7	19	1	AI570374	to78f07.x
C 133	10.6	55.8	24	11	A2640795	1M0503D04	C 206	10.2	53.7	19	5	CF314442	HD--02-P1
C 134	10.6	55.8	24	11	A2789161	2M0036A15	C 207	10.2	53.7	19	11	AZ447197	1M0244A08
C 135	10.6	55.8	24	11	A2822871	2M0096B05	C 208	10.2	53.7	19	11	AZ782026	2M0021I23
C 136	10.6	55.8	24	11	A2823931	1M0098F17	C 209	10.2	53.7	19	11	AZ819494	2M0091I10
C 137	10.6	55.8	25	1	AA912548	o135c01.s	C 210	10.2	53.7	19	11	AZ822954	2M0096I10
C 138	10.6	55.8	25	11	A2348233	1M0084G04	C 211	10.2	53.7	19	11	AZ824929	2M0099P16
C 139	10.6	55.8	25	11	A2350753	1M0088M20	C 212	10.2	53.7	19	11	AZ967656	2M0238M09
C 140	10.6	55.8	25	11	A2510562	1M0355F11	C 213	10.2	53.7	20	5	CF338875	RCL1--03-
C 141	10.6	55.8	25	11	A2602480	1M0421F16	C 214	10.2	53.7	20	11	AZ447706	1M0245C06
C 142	10.6	55.8	25	11	A2780325	2M0017N06	C 215	10.2	53.7	20	11	AZ475834	1M0294N10
C 143	10.6	55.8	25	11	A2853337	1M0156A04	C 216	10.2	53.7	20	11	AZ642891	1M0506D12
C 144	10.6	55.8	25	11	A2873581	2M0187G19	C 217	10.2	53.7	20	11	AZ772707	1M0583L18
C 145	10.6	55.8	25	12	CG707197	1119001E1	C 218	10.2	53.7	20	11	AZ833537	2M0115M09
C 146	10.6	55.8	26	4	BX626114	BX626114	C 219	10.2	53.7	20	11	AZ862316	2M0169I11
C 147	10.6	55.8	26	5	CF309675	ABF--03-P	C 220	10.2	53.7	20	13	CL660020	PR10135d
C 148	10.6	55.8	26	11	A2307654	1M0009F22	C 221	10.2	53.7	20	14	DX081956	KBF0805A2
C 149	10.6	55.8	26	11	A2363822	1M0109P03	C 222	10.2	53.7	21	11	AZ589393	1M0398A20
C 150	10.6	55.8	26	11	A2462959	1M0271G04	C 223	10.2	53.7	21	11	AZ595941	2M0227C07
C 151	10.6	55.8	26	11	A2468564	1M0281G10	C 224	10.2	53.7	21	11	AZ959441	2M0227C07
C 152	10.6	55.8	26	11	A2810458	2M0076C02	C 225	10.2	53.7	21	14	DU835421	KBF05016K0
C 153	10.6	55.8	26	11	A2861534	2M0168K19	C 226	10.2	53.7	22	1	AA996014	o826d08.s
C 154	10.6	55.8	26	13	CW982257	KBF007C1	C 227	10.2	53.7	22	11	AA955969	ow30h02.s
C 155	10.6	55.8	27	11	A2355810	1M0095G10	C 228	10.2	53.7	22	13	AZ982662	2M0263J06
C 156	10.6	55.8	27	11	A2416143	1M0193G14	C 229	10.2	53.7	22	14	DU835197	KBF05016D0
C 157	10.6	55.8	27	11	A2426894	1M0208P03	C 230	10.2	53.7	22	14	TA137G03P	T. brucei
C 158	10.6	55.8	27	11	A2604434	1M0425I18	C 231	10.2	53.7	23	1	AM044554	AM044554
C 159	10.6	55.8	27	11	A2649949	1M0519P18	C 232	10.2	53.7	23	5	CF333152	JMT--01-O
C 160	10.6	55.8	27	11	A2997581	2M0284J09	C 233	10.2	53.7	23	9	DR064698	ip85c02.g
C 161	10.6	55.8	28	1	AI821537	zt38c07.x	C 234	10.2	53.7	23	11	AZ309863	1M0017P09
C 162	10.6	55.8	28	4	BX629284	BX629284	C 235	10.2	53.7	23	11	AZ488138	1M0318B13
C 163	10.6	55.8	28	11	A2403204	1M0170G19	C 236	10.2	53.7	23	11	AZ611718	1M0438B18
C 164	10.6	55.8	28	11	A2459967	1M0265D08	C 237	10.2	53.7	23	11	AZ611718	1M0438B18
C 165	10.6	55.8	28	11	A2486749	1M0315G02	C 238	10.2	53.7	23	11	AZ945654	2M0207C10

C 239	10.2	53.7	23	14	DX036713	312	10	52.6	21	14	TA71B09Q	AL457696 T. brucei
240	10.2	53.7	23	14	TA173D05P	313	10	52.6	22	1	AJ732535	AJ732535
241	10.2	53.7	24	14	TA356F10P	314	10	52.6	22	5	CF282319	CF282319 AJETL--09
242	10.2	53.7	24	5	CF340367	315	10	52.6	22	11	AZ656873	AZ656873 1M0532M09
243	10.2	53.7	24	8	CV055483	316	10	52.6	22	11	AZ986234	AZ986234 2M0268C19
244	10.2	53.7	24	14	TA178P08P	317	10	52.6	22	5	CF332288	CF332288 NACL--08-
245	10.2	53.7	25	1	A13633940	318	10	52.6	23	11	DV226161	DV226161 EST-AR113
246	10.2	53.7	25	1	A1416870	319	10	52.6	23	11	AZ329120	AZ329120 1M053A14
247	10.2	53.7	25	1	A1443365	320	10	52.6	23	11	AZ764532	AZ764532 1M0560M18
248	10.2	53.7	25	1	A1648460	321	10	52.6	24	5	CF304020	CF304020 ABP1--03-
249	10.2	53.7	25	9	DR074081	322	10	52.6	24	11	AZ387313	AZ387313 1M0146E08
250	10.2	53.7	25	11	AZ486714	323	10	52.6	24	11	AZ656029	AZ656029 1M053A018
251	10.2	53.7	25	11	AZ6332343	324	10	52.6	24	11	AZ806300	AZ806300 2M0068F13
252	10.2	53.7	25	11	AZ795708	325	10	52.6	24	11	AZ844396	AZ844396 2M0143B22
253	10.2	53.7	25	11	AZ810919	326	10	52.6	24	14	TA363E08P	TA363E08P
254	10.2	53.7	25	11	AZ820085	327	10	52.6	25	1	AM046161	AM046161 AM046161
255	10.2	53.7	25	11	AZ820085	328	10	52.6	25	11	AZ646830	AZ646830 1M0513104
256	10.2	53.7	25	11	AZ950326	329	10	52.6	25	13	CZ918376	CZ918376 4021009B0
257	10.2	53.7	25	13	CZ908046	330	10	52.6	26	1	AJ661750	AJ661750 AJ661750
258	10.2	53.7	25	13	CL681025	331	10	52.6	26	2	BM397648	BM397648 5009-0-35
259	10.2	53.7	25	14	DX055363	332	10	52.6	26	11	AZ767933	AZ767933 1M0567B10
260	10.2	53.7	25	14	AG191246	333	10	52.6	26	14	DU753579	DU753579 ASNF3233
261	10.2	53.7	25	14	TA232G09Q	334	10	52.6	27	2	BM395101	BM395101 50072-2-7
262	10.2	53.7	25	14	TA232H10Q	335	10	52.6	27	11	AZ453355	AZ453355 1M0272E09
263	10.2	53.7	25	14	TA261B03P	336	10	52.6	27	11	AZ473702	AZ473702 1M0289A14
264	10.2	53.7	26	1	A5588210	337	10	52.6	27	11	DU829541	DU829541 KB-S005B2
265	10.2	53.7	26	11	AZ431644	338	10	52.6	27	14	DX072767	DX072767 KB-S008202
266	10.2	53.7	26	11	AZ447254	339	10	52.6	28	1	AJ351154	AJ351154 qt11g11.x
267	10.2	53.7	26	11	AZ864944	340	10	52.6	28	1	A1445347	A1445347 tj19b11.x
268	10.2	53.7	26	13	CL659570	341	10	52.6	28	1	A1597957	A1597957 t604f01.x
269	10.2	53.7	26	14	DX045718	342	10	52.6	28	1	AJ694147	AJ694147 AJ694147
270	10.2	53.7	26	14	TA319G03Q	343	10	52.6	28	11	AZ345466	AZ345466 1M0080N10
271	10.2	53.7	27	11	AZ453213	344	10	52.6	28	11	AZ614443	AZ614443 1M0433F15
272	10.2	53.7	27	11	AZ495213	345	10	52.6	28	11	AZ785207	AZ785207 2M0028P12
273	10.2	53.7	27	11	AZ765547	346	10	52.6	29	11	AZ764536	AZ764536 1M0560A24
274	10.2	53.7	27	14	TA28G07Q	347	10	52.6	29	11	AZ799171	AZ799171 2M0058F14
275	10.2	53.7	28	1	A17833508	348	10	52.6	29	11	AZ833672	AZ833672 2M0115122
276	10.2	53.7	28	11	AZ309062	349	10	52.6	30	11	AZ864869	AZ864869 2M0174M09
277	10.2	53.7	28	11	AZ363489	350	10	52.6	30	14	DU767213	DU767213 ANTIW8891
278	10.2	53.7	28	11	AZ649613	351	10	52.6	30	14	TA28A09P	TA28A09P
279	10.2	53.7	28	11	AZ792783	352	9.8	51.6	15	1	A1209036	A1209036 qg18g10.x
280	10.2	53.7	28	11	AZ937148	353	9.8	51.6	17	1	AJ666397	AJ666397 AJ666397
281	10.2	53.7	28	11	AZ957207	354	9.8	51.6	19	1	A1431460	A1431460 th40c01.x
282	10.2	53.7	28	11	AZ986927	355	9.8	51.6	19	1	A1719958	A1719958 as41d06.x
283	10.2	53.7	28	12	CL685975	356	9.8	51.6	19	5	CF298891	CF298891 7LEAF--02
284	10.2	53.7	28	13	CL663977	357	9.8	51.6	19	5	CF298891	CF298891 7LEAF--02
285	10.2	53.7	28	13	CL68485	358	9.8	51.6	19	11	AZ775541	AZ775541 2M0008H17
286	10.2	53.7	28	14	TA186G09P	359	9.8	51.6	19	11	AZ949434	AZ949434 2M0212K23
287	10.2	53.7	28	14	TA37A10P	360	9.8	51.6	20	11	AZ465909	AZ465909 1M0276112
288	10.2	53.7	29	5	CF309854	361	9.8	51.6	20	11	AZ619034	AZ619034 1M0451111
289	10.2	53.7	29	11	AZ453011	362	9.8	51.6	20	11	AZ785534	AZ785534 2M0029A05
290	10.2	53.7	29	11	AZ949281	363	9.8	51.6	20	11	AZ846437	AZ846437 2M0146B10
291	10.2	53.7	29	11	AZ992478	364	9.8	51.6	20	11	AZ864576	AZ864576 2M0174C15
292	10.2	53.7	29	13	CL660119	365	9.8	51.6	20	11	AZ957966	AZ957966 2M0225I01
293	10.2	53.7	30	1	AM047980	366	9.8	51.6	21	1	AJ692277	AJ692277 AJ692277
294	10.2	53.7	30	3	BQ590438	367	9.8	51.6	21	11	AZ387199	AZ387199 1M0146P20
295	10.2	53.7	30	11	AZ463319	368	9.8	51.6	21	11	AZ442444	AZ442444 1M0236N21
296	10.2	53.7	30	11	AZ501729	369	9.8	51.6	21	11	AZ657586	AZ657586 1M0532D24
297	10.2	53.7	30	11	AZ633504	370	9.8	51.6	21	11	AZ856540	AZ856540 2M0161D03
298	10.2	53.7	30	11	AZ634665	371	9.8	51.6	21	11	AZ861360	AZ861360 2M0167G17
299	10.2	53.7	30	11	AZ779367	372	9.8	51.6	21	13	CL669293	CL669293 PRI015A_B
300	10.2	53.7	30	14	DX062633	373	9.8	51.6	22	1	AA931067	AA931067 om87a08.s
301	10.2	53.7	30	14	DX062633	374	9.8	51.6	22	1	A1274595	A1274595 qv11b07.x
302	10.2	53.7	30	14	DX062633	375	9.8	51.6	22	1	A1608652	A1608652 tw17h05.x
303	10.2	53.7	30	14	DX062633	376	9.8	51.6	22	11	AZ828663	AZ828663 2M0105I14
304	10.2	53.7	30	14	DX062633	377	9.8	51.6	22	11	AZ837879	AZ837879 2M0133A22
305	10.2	53.7	30	14	DX062633	378	9.8	51.6	22	14	DX080981	DX080981 KBR093L2
306	10.2	53.7	30	14	DX062633	379	9.8	51.6	22	14	TA245E10P	TA245E10P
307	10.2	53.7	30	14	DX062633	380	9.8	51.6	22	11	AZ305188	AZ305188 1M0005C17
308	10.2	53.7	30	14	DX062633	381	9.8	51.6	22	11	AZ615086	AZ615086 1M0444C14
309	10.2	53.7	30	14	DX062633	382	9.8	51.6	22	11	AZ818371	AZ818371 2M0088C21
310	10.2	53.7	30	14	DX062633	383	9.8	51.6	22	11	AZ819376	AZ819376 2M0089F23
311	10.2	53.7	30	14	DX062633	384	9.8	51.6	22	11	AZ965976	AZ965976 2M0236G14

C 385	9.8	51.6	23	14	DX018712	DX018712 KBrB011J1	458	9.6	50.5	22	3	BQ585098	BQ585098 E011826-0
C 386	9.8	51.6	23	14	DX060572	DX060572 KBrB066N1	459	9.6	50.5	22	5	CF281903	CF281903 14ETL--09
C 387	9.8	51.6	23	14	CT010976	CT010976 KBrH118E1	460	9.6	50.5	22	11	AZ307488	AZ307488 1M0009B13
C 388	9.8	51.6	24	5	CF295238	CF295238 3DGS--05	C 461	9.6	50.5	22	11	AZ589449	AZ589449 1M0398M24
C 389	9.8	51.6	24	14	TA155F12Q	TA155F12Q T. brucei	462	9.6	50.5	22	11	AZ603158	AZ603158 1M0422L13
C 390	9.8	51.6	24	14	TA185C06P	TA185C06P T. brucei	463	9.6	50.5	22	11	AZ606880	AZ606880 1M0429H03
C 391	9.8	51.6	24	14	TA235H03Q	TA235H03Q T. brucei	C 464	9.6	50.5	22	11	AZ779122	AZ779122 2M0015M03
C 392	9.8	51.6	25	1	A1041825	A1041825 oy34b05.x	465	9.6	50.5	22	13	CL655007	CL655007 PR10122a
C 393	9.8	51.6	25	1	A1453394	A1453394 t3j7g02.x	466	9.6	50.5	23	11	AZ374746	AZ374746 1M0127D15
C 394	9.8	51.6	25	1	A1471676	A1471676 t199d02.x	467	9.6	50.5	23	11	AZ410218	AZ410218 1M0182F23
C 395	9.8	51.6	25	1	A1682835	A1682835 wc66h10.x	C 468	9.6	50.5	23	11	AZ439451	AZ439451 1M0230C09
C 396	9.8	51.6	25	1	A1915575	A1915575 tr40g09.x	469	9.6	50.5	23	11	AZ647047	AZ647047 1M0513B22
C 397	9.8	51.6	25	11	AZ450283	AZ450283 1M0249002	C 470	9.6	50.5	23	11	AZ659712	AZ659712 1M0537J18
C 398	9.8	51.6	25	11	AZ500456	AZ500456 1M0338017	C 471	9.6	50.5	23	11	AZ855661	AZ855661 2M0159J17
C 399	9.8	51.6	25	11	AZ6311099	AZ6311099 1M0436K13	C 472	9.6	50.5	23	11	AZ949214	AZ949214 2M0212Q05
C 400	9.8	51.6	25	11	AZ945526	AZ945526 2M0206L22	473	9.6	50.5	23	11	AZ971749	AZ971749 2M0245C21
C 401	9.8	51.6	25	13	CZ918500	CZ918500 4021009F1	474	9.6	50.5	24	1	AJ668266	AJ668266 AJ668266
C 402	9.8	51.6	25	14	DX046122	DX046122 KBrB047K1	C 475	9.6	50.5	24	5	CF326142	CF326142 JMT1--05-
C 403	9.8	51.6	26	11	AZ424207	AZ424207 1M0203N07	476	9.6	50.5	24	11	AZ845302	AZ845302 2M0145I06
C 404	9.8	51.6	26	11	AZ484118	AZ484118 1M0245C10	477	9.6	50.5	25	1	A1467995	A1467995 t39e07.x
C 405	9.8	51.6	26	11	AZ512846	AZ512846 1M0358N07	C 478	9.6	50.5	25	1	A1571526	A1571526 tr85C03.x
C 406	9.8	51.6	26	11	AZ641136	AZ641136 1M0503E01	C 479	9.6	50.5	25	11	AZ406180	AZ406180 1M0175M18
C 407	9.8	51.6	26	13	CZ919340	CZ919340 4021012G0	480	9.6	50.5	25	11	AZ431597	AZ431597 1M0216C10
C 408	9.8	51.6	26	14	DU831494	DU831494 KBrS008J0	481	9.6	50.5	25	11	AZ438688	AZ438688 1M0228H19
C 409	9.8	51.6	26	14	AJ840729	AJ840729 Arabidops	482	9.6	50.5	25	11	AZ620217	AZ620217 1M0452B23
C 410	9.8	51.6	26	14	TA97C06P	TA97C06P T. brucei	483	9.6	50.5	25	11	AZ776699	AZ776699 2M0010L02
C 411	9.8	51.6	27	9	D17088	D17088 D17088 Kise	C 484	9.6	50.5	25	11	AZ796046	AZ796046 2M0051B17
C 412	9.8	51.6	27	11	AZ948983	AZ948983 2M0212C15	485	9.6	50.5	25	11	AZ937578	AZ937578 2M0195L17
C 413	9.8	51.6	27	11	AZ970595	AZ970595 2M0243I18	486	9.6	50.5	25	13	CL685316	CL685316 PR10140d
C 414	9.8	51.6	27	14	CT014304	CT014304 KBrH122P2	487	9.6	50.5	25	14	TA185B02Q	TA185B02Q T. brucei
C 415	9.8	51.6	27	14	TA356E04P	TA356E04P T. brucei	488	9.6	50.5	25	14	TA356H06P	TA356H06P T. brucei
C 416	9.8	51.6	28	1	A8660464	A8660464 aj85a02.s	489	9.6	50.5	26	11	AZ955924	AZ955924 2M0222P10
C 417	9.8	51.6	28	1	A8954651	A8954651 om95b06.s	C 490	9.6	50.5	26	14	DU833380	DU833380 KBrS012A0
C 418	9.8	51.6	28	1	A1087295	A1087295 oz77h02.x	491	9.6	50.5	26	14	AG130159	AG130159 Pan trogl
C 419	9.8	51.6	28	1	A1174332	A1174332 anl7d02.s	492	9.6	50.5	27	1	AJ649606	AJ649606 AJ649606
C 420	9.8	51.6	28	1	A1306628	A1306628 qn45h01.x	C 493	9.6	50.5	27	1	AU259022	AU259022 AU259022
C 421	9.8	51.6	28	1	A1357341	A1357341 qy12e10.x	494	9.6	50.5	27	2	BM399490	BM399490 5009-058
C 422	9.8	51.6	28	1	A1446622	A1446622 t325d04.x	495	9.6	50.5	27	5	CD530450	CD530450 06F11 Ara
C 423	9.8	51.6	28	1	A1499167	A1499167 t05h03.x	496	9.6	50.5	27	11	AZ506426	AZ506426 1M0347M04
C 424	9.8	51.6	28	1	A1667101	A1667101 fc37f08.x	497	9.6	50.5	27	11	AZ622014	AZ622014 1M0455I03
C 425	9.8	51.6	28	1	A1745328	A1745328 tr21901.x	498	9.6	50.5	27	11	AZ835935	AZ835935 2M0130K19
C 426	9.8	51.6	28	11	AZ802448	AZ802448 2M0061B20	C 499	9.6	50.5	27	11	AZ979506	AZ979506 2M0256A13
C 427	9.8	51.6	28	11	AZ853408	AZ853408 2M0156P01	500	9.6	50.5	27	12	CG713231	CG713231 1119031A0
C 428	9.8	51.6	29	1	AM075309	AM075309 AM075309	501	9.6	50.5	27	13	CT021050	CT021050 KBrH136a
C 429	9.8	51.6	29	11	AZ391891	AZ391891 1M0154F14	C 502	9.6	50.5	27	14	TA287F07P	TA287F07P T. brucei
C 430	9.8	51.6	29	11	AZ432529	AZ432529 1M0218C04	503	9.6	50.5	28	1	A1628556	A1628556 cy95d11.x
C 431	9.8	51.6	29	11	AZ777445	AZ777445 2M0011C19	504	9.6	50.5	28	1	A1687742	A1687742 tp93h01.x
C 432	9.8	51.6	29	11	AZ801486	AZ801486 2M0059P23	C 506	9.6	50.5	28	1	A1918417	A1918417 tr96d10.x
C 433	9.8	51.6	29	11	AZ862317	AZ862317 2M0169J13	C 507	9.6	50.5	28	13	CW982427	CW982427 KBrH007G1
C 434	9.8	51.6	29	12	CG769372	CG769372 TC852.3.A	C 508	9.6	50.5	28	13	CW982427	CW982427 KBrH007G1
C 435	9.8	51.6	29	13	CZ907899	CZ907899 4018001A0	C 509	9.6	50.5	28	13	CZ907021	CZ907021 4011004G0
C 436	9.8	51.6	29	14	DU829331	DU829331 KBrS004L1	C 510	9.6	50.5	29	1	AJ673541	AJ673541 AJ673541
C 437	9.8	51.6	29	14	TA239G06Q	TA239G06Q T. brucei	C 511	9.6	50.5	29	5	CJ054334	CJ054334 CJ054334
C 438	9.8	51.6	30	11	AZ406515	AZ406515 1M0175I14	C 512	9.6	50.5	29	9	DN953812	DN953812 it64g12.9
C 439	9.8	51.6	30	11	AZ787677	AZ787677 2M0034H17	C 513	9.6	50.5	29	11	AZ321120	AZ321120 1M0041H16
C 440	9.8	51.6	30	13	CZ913610	CZ913610 4013003D0	514	9.6	50.5	29	11	AZ602874	AZ602874 1M0421B21
C 441	9.8	51.6	30	14	DX080575	DX080575 KBrB093C1	515	9.6	50.5	29	11	AZ6641783	AZ6641783 1M0504E06
C 442	9.8	51.6	30	14	TA183B05P	TA183B05P T. brucei	516	9.6	50.5	29	11	AZ956998	AZ956998 2M0223P12
C 443	9.8	51.6	30	14	TA211H11Q	TA211H11Q T. brucei	C 517	9.6	50.5	29	14	DU835009	DU835009 KBrS015M0
C 444	9.6	50.5	19	1	A1537209	A1537209 tp06f07.x	518	9.6	50.5	29	14	DX056930	DX056930 KBrB062A0
C 445	9.6	50.5	19	1	A1690354	A1690354 tx14f06.x	519	9.6	50.5	30	8	CW999848	CW999848 iv53e08.g
C 446	9.6	50.5	19	1	A1807936	A1807936 wf52e09.x	520	9.6	50.5	30	11	AZ408503	AZ408503 1M0179P12
C 447	9.6	50.5	19	11	AZ654214	AZ654214 1M0528H13	521	9.6	50.5	30	11	AZ604126	AZ604126 1M0423O13
C 448	9.6	50.5	20	8	CN752083	CN752083 ApHL3SD-X	522	9.6	50.5	30	13	CZ558878	CZ558878 M0051780
C 449	9.6	50.5	20	11	AZ627848	AZ627848 1M0474G14	523	9.6	50.5	30	13	CZ559054	CZ559054 M0053020
C 450	9.6	50.5	20	11	AZ818394	AZ818394 2M0088G23	C 524	9.6	50.5	30	13	CZ919131	CZ919131 KBrS013A1
C 451	9.6	50.5	20	14	DU834060	DU834060 KBrS013F1	C 525	9.6	50.5	30	14	DU833917	DU833917 KBrS013A1
C 452	9.6	50.5	20	14	DX030114	DX030114 KBrB026I1	526	9.6	50.5	30	14	DX063780	DX063780 KBrB071A2
C 453	9.6	50.5	21	4	BX568462	BX568462 BX568462	C 527	9.6	50.5	16	1	AA968729	AA968729 or69h11.s
C 454	9.6	50.5	21	11	AZ443821	AZ443821 1M0238I07	528	9.6	50.5	16	1	A1684114	A1684114 tx78d02.x
C 455	9.6	50.5	21	11	AZ472401	AZ472401 1M0287C07	C 529	9.6	50.5	19	1	AG190497	AG190497 Pan trogl
C 456	9.6	50.5	21	14	AG190497	AG190497 Pan trogl	C 530	9.6	50.5	19	1	A1364573	A1364573 qw37g03.x
C 457	9.6	50.5	22	1	A1707945	A1707945 as34g10.x							

C 531	9.4	49.5	9.4	49.5	604	9.4	49.5	26	11	AZ588958	1M0397B09
C 532	9.4	49.5	9.4	49.5	605	9.4	49.5	26	13	CZ914182	401300SH0
C 533	9.4	49.5	9.4	49.5	C 606	9.4	49.5	26	14	AJ194390	Pan trogl
C 534	9.4	49.5	9.4	49.5	C 607	9.4	49.5	26	14	AJ599130	Arabidops
C 535	9.4	49.5	9.4	49.5	C 608	9.4	49.5	27	8	CX009757	io42e08.b
C 536	9.4	49.5	9.4	49.5	C 609	9.4	49.5	27	11	AZ403394	1M0171109
C 537	9.4	49.5	9.4	49.5	C 610	9.4	49.5	27	11	AZ403394	1M0171109
C 538	9.4	49.5	9.4	49.5	C 611	9.4	49.5	27	11	AZ479687	1M0300R02
C 539	9.4	49.5	9.4	49.5	C 612	9.4	49.5	27	11	AZ768325	1M0568F17
C 540	9.4	49.5	9.4	49.5	C 613	9.4	49.5	27	11	AZ840204	2M0136H08
C 541	9.4	49.5	9.4	49.5	C 614	9.4	49.5	27	11	AZ951944	2M0216004
C 542	9.4	49.5	9.4	49.5	C 615	9.4	49.5	28	1	A864806	oh02h06.s
C 543	9.4	49.5	9.4	49.5	C 616	9.4	49.5	28	1	A886956	oi14e09.s
C 544	9.4	49.5	9.4	49.5	C 617	9.4	49.5	28	1	A905471	ok01f11.s
C 545	9.4	49.5	9.4	49.5	C 618	9.4	49.5	28	1	A911003	ok57f12.s
C 546	9.4	49.5	9.4	49.5	C 619	9.4	49.5	28	1	A1355566	qt75g02.x
C 547	9.4	49.5	9.4	49.5	C 620	9.4	49.5	28	1	A1377008	tc34h10.x
C 548	9.4	49.5	9.4	49.5	C 621	9.4	49.5	28	1	A1529170	ui66b12.y
C 549	9.4	49.5	9.4	49.5	C 622	9.4	49.5	28	1	A1613531	tw22h06.x
C 550	9.4	49.5	9.4	49.5	C 623	9.4	49.5	28	1	A1623372	tw18e04.x
C 551	9.4	49.5	9.4	49.5	C 624	9.4	49.5	28	1	A1633014	tz33d07.x
C 552	9.4	49.5	9.4	49.5	C 625	9.4	49.5	28	1	A1687017	tp81h11.x
C 553	9.4	49.5	9.4	49.5	C 626	9.4	49.5	28	1	AJ682978	AJ682978
C 554	9.4	49.5	9.4	49.5	C 627	9.4	49.5	28	1	AM048443	AM048443
C 555	9.4	49.5	9.4	49.5	C 628	9.4	49.5	28	11	AZ342196	1M0075F07
C 556	9.4	49.5	9.4	49.5	C 629	9.4	49.5	28	11	AZ430095	1M0214U19
C 557	9.4	49.5	9.4	49.5	C 630	9.4	49.5	28	11	AZ659656	1M0537K08
C 558	9.4	49.5	9.4	49.5	C 631	9.4	49.5	28	11	AZ828724	2M0105E24
C 559	9.4	49.5	9.4	49.5	C 632	9.4	49.5	28	11	AZ833779	2M0116A09
C 560	9.4	49.5	9.4	49.5	C 633	9.4	49.5	28	14	AG192430	Pan trogl
C 561	9.4	49.5	9.4	49.5	C 634	9.4	49.5	29	11	AZ313334	1M0029D03
C 562	9.4	49.5	9.4	49.5	C 635	9.4	49.5	29	11	AZ479604	1M0300E21
C 563	9.4	49.5	9.4	49.5	C 636	9.4	49.5	29	11	AZ786433	1M0537O24
C 564	9.4	49.5	9.4	49.5	C 637	9.4	49.5	29	11	AZ795441	2M0049K12
C 565	9.4	49.5	9.4	49.5	C 638	9.4	49.5	29	14	DU835101	KB-S016A0
C 566	9.4	49.5	9.4	49.5	C 639	9.4	49.5	30	11	DZ5861	HUMGS04239
C 567	9.4	49.5	9.4	49.5	C 640	9.4	49.5	30	11	AZ375563	1M0128P24
C 568	9.4	49.5	9.4	49.5	C 641	9.4	49.5	30	11	AZ995340	2M0281E11
C 569	9.4	49.5	9.4	49.5	C 642	9.4	49.5	30	13	AZ480720	eo2954-5p
C 570	9.4	49.5	9.4	49.5	C 643	9.4	49.5	30	14	TA172F01Q	AI73531 T. brucei
C 571	9.4	49.5	9.4	49.5	C 644	9.4	49.5	16	1	A1564678	tg78g03.x
C 572	9.4	49.5	9.4	49.5	C 645	9.2	48.4	18	14	DU642495	Ciuffi-HI
C 573	9.4	49.5	9.4	49.5	C 646	9.2	48.4	18	14	DU642495	Ciuffi-HI
C 574	9.4	49.5	9.4	49.5	C 647	9.2	48.4	19	1	A1758301	ty06a07.x
C 575	9.4	49.5	9.4	49.5	C 648	9.2	48.4	19	1	A1811474	t43c04.x
C 576	9.4	49.5	9.4	49.5	C 649	9.2	48.4	19	11	AZ343228	1M0076M05
C 577	9.4	49.5	9.4	49.5	C 650	9.2	48.4	19	11	AZ512762	1M0358M04
C 578	9.4	49.5	9.4	49.5	C 651	9.2	48.4	19	11	AZ646713	1M0512D20
C 579	9.4	49.5	9.4	49.5	C 652	9.2	48.4	19	11	AZ761834	1M0556E19
C 580	9.4	49.5	9.4	49.5	C 653	9.2	48.4	19	13	CL657666	PR1012a.H
C 581	9.4	49.5	9.4	49.5	C 654	9.2	48.4	20	11	AZ388212	1M0148A10
C 582	9.4	49.5	9.4	49.5	C 655	9.2	48.4	20	1	DR063899	ip71e12.g
C 583	9.4	49.5	9.4	49.5	C 656	9.2	48.4	21	10	DV225120	EST-AR103
C 584	9.4	49.5	9.4	49.5	C 657	9.2	48.4	21	10	DV225120	EST-AR103
C 585	9.4	49.5	9.4	49.5	C 658	9.2	48.4	21	11	AZ321746	1M0042N20
C 586	9.4	49.5	9.4	49.5	C 659	9.2	48.4	21	11	AZ399828	1M0165A23
C 587	9.4	49.5	9.4	49.5	C 660	9.2	48.4	21	11	AZ632964	1M0487H22
C 588	9.4	49.5	9.4	49.5	C 661	9.2	48.4	22	1	A1582080	ar96b07.x
C 589	9.4	49.5	9.4	49.5	C 662	9.2	48.4	22	1	A1971767	wv28a05.x
C 590	9.4	49.5	9.4	49.5	C 663	9.2	48.4	22	11	AZ640656	1M0502K14
C 591	9.4	49.5	9.4	49.5	C 664	9.2	48.4	22	11	AZ958287	2M0225G02
C 592	9.4	49.5	9.4	49.5	C 665	9.2	48.4	23	2	BG924553	HNC37-1-H
C 593	9.4	49.5	9.4	49.5	C 666	9.2	48.4	23	11	AZ499076	1M0336H08
C 594	9.4	49.5	9.4	49.5	C 667	9.2	48.4	23	11	AZ593207	1M0402N20
C 595	9.4	49.5	9.4	49.5	C 668	9.2	48.4	23	11	AZ595375	1M0407P19
C 596	9.4	49.5	9.4	49.5	C 669	9.2	48.4	23	11	AZ610186	1M0435A21
C 597	9.4	49.5	9.4	49.5	C 670	9.2	48.4	23	11	AZ774668	2M0004N08
C 598	9.4	49.5	9.4	49.5	C 671	9.2	48.4	23	11	AZ600832	1M0418014
C 599	9.4	49.5	9.4	49.5	C 672	9.2	48.4	25	1	A1432500	th35h06.x
C 600	9.4	49.5	9.4	49.5	C 673	9.2	48.4	25	10	DW373978	EST-AR042
C 601	9.4	49.5	9.4	49.5	C 674	9.2	48.4	25	11	AZ41038	1M0232P20
C 602	9.4	49.5	9.4	49.5	C 675	9.2	48.4	25	11	AZ468549	1M0281D10
C 603	9.4	49.5	9.4	49.5	C 676	9.2	48.4	25	11	AZ620092	1M0452U07

C 677	9.2	48.4	25	11	AZ781710	AZ781710 2M0021E15	C 750	9	47.4	19	11	AZ247731	1M0209G1.9
C 678	9.2	48.4	25	11	BH146175	BH146175 BG02743-5	C 751	9	47.4	19	11	AZ427731	AZ427731 1M0209N1.9
C 679	9.2	48.4	25	13	CZ909373	CZ909373 4018009B0	C 752	9	47.4	19	11	AZ427750	AZ427750 1M0229B1.5
C 680	9.2	48.4	26	11	AZ768557	AZ768557 1M0568B04	C 753	9	47.4	19	11	AZ446934	AZ446934 1M0243N01
C 681	9.2	48.4	26	11	AZ942099	AZ942099 2M0202C09	C 754	9	47.4	19	11	AZ447234	AZ447234 1M0244L16
C 682	9.2	48.4	26	14	AG188964	AG188964 Fan trogl	C 755	9	47.4	19	11	AZ447245	AZ447245 1M0244A22
C 683	9.2	48.4	27	11	AZ399752	AZ399752 1M0165D15	C 756	9	47.4	19	11	AZ466785	AZ466785 1M0277A16
C 684	9.2	48.4	27	11	AZ784820	AZ784820 2M0028N04	C 757	9	47.4	19	11	AZ468226	AZ468226 1M0281D10
C 685	9.2	48.4	27	11	AZ842796	AZ842796 2M0141120	C 758	9	47.4	19	11	AZ478905	AZ478905 1M0299E18
C 686	9.2	48.4	27	12	CG728385	CG728385 1119100A1	C 759	9	47.4	19	11	AZ481469	AZ481469 1M0303B15
C 687	9.2	48.4	28	1	A1434397	A1434397 t148R06.x	C 760	9	47.4	19	11	AZ493581	AZ493581 1M0328A24
C 688	9.2	48.4	28	1	A1444428	A1444428 fD38C12.x	C 761	9	47.4	19	11	AZ499200	AZ499200 1M0336O22
C 689	9.2	48.4	28	1	A1544609	A1544609 fD76603.x	C 762	9	47.4	19	11	AZ579189	AZ579189 1M0363I12
C 690	9.2	48.4	28	1	A1686998	A1686998 tp81e01.x	C 763	9	47.4	19	11	AZ587841	AZ587841 1M0395J14
C 691	9.2	48.4	28	11	AZ584848	AZ584848 1M0389I13	C 764	9	47.4	19	11	AZ611179	AZ611179 1M0436B01
C 692	9.2	48.4	28	11	AZ594339	AZ594339 1M0406A21	C 765	9	47.4	19	11	AZ611509	AZ611509 1M0437E21
C 693	9.2	48.4	28	11	AZ594339	AZ594339 1M0406A21	C 766	9	47.4	19	11	AZ615843	AZ615843 1M0445E23
C 694	9.2	48.4	28	13	CZ907925	CZ907925 4018001B0	C 767	9	47.4	19	11	AZ618258	AZ618258 1M0449G23
C 695	9.2	48.4	28	14	TAISO08Y	AL057272 Drosophil	C 768	9	47.4	19	11	AZ625211	AZ625211 1M0464P22
C 696	9.2	48.4	28	14	CNS0812P	AL464095 T. brucei	C 769	9	47.4	19	11	AZ625605	AZ625605 1M0465D17
C 697	9.2	48.4	29	1	AM043404	AM043404	C 770	9	47.4	19	11	AZ643205	AZ643205 1M0489D19
C 698	9.2	48.4	29	11	AZ406476	AZ406476 1M0175B15	C 771	9	47.4	19	11	AZ648703	AZ648703 1M0517A20
C 699	9.2	48.4	29	11	AZ438509	AZ438509 1M0228G08	C 772	9	47.4	19	11	AZ649856	AZ649856 1M0519O07
C 700	9.2	48.4	29	11	AZ774255	AZ774255 2M0003J24	C 773	9	47.4	19	11	AZ650212	AZ650212 1M0520G13
C 701	9.2	48.4	29	11	AZ783480	AZ783480 2M0025F14	C 774	9	47.4	19	11	AZ654733	AZ654733 1M0529A09
C 702	9.2	48.4	29	11	AZ805819	AZ805819 2M0067K19	C 775	9	47.4	19	11	AZ654842	AZ654842 1M0529A20
C 703	9.2	48.4	29	11	AZ815922	AZ815922 2M0084L06	C 776	9	47.4	19	11	AZ656937	AZ656937 1M0532K13
C 704	9.2	48.4	29	11	AZ854411	AZ854411 2M0158B05	C 777	9	47.4	19	11	AZ657564	AZ657564 1M0533P18
C 705	9.2	48.4	29	11	BH856361	BH856361 SALK_0798	C 778	9	47.4	19	11	AZ764495	AZ764495 1M0560G06
C 706	9.2	48.4	29	12	BZ595262	BZ595262 SALK_0863	C 779	9	47.4	19	11	AZ764500	AZ764500 1M0560K06
C 707	9.2	48.4	29	13	CZ908389	CZ908389 4018002H0	C 780	9	47.4	19	11	AZ764526	AZ764526 1M0560J15
C 708	9.2	48.4	29	13	CL653182	CL653182 PRI0116d	C 781	9	47.4	19	11	AZ769239	AZ769239 1M0566K09
C 709	9.2	48.4	30	7	BE295129	BE295129 601173573	C 782	9	47.4	19	11	AZ783420	AZ783420 2M0025D07
C 710	9.2	48.4	30	11	AZ456295	AZ456295 1M0259J04	C 783	9	47.4	19	11	AZ786434	AZ786434 2M0031M24
C 711	9.2	48.4	30	11	AZ801555	AZ801555 2M0060M01	C 784	9	47.4	19	11	AZ795057	AZ795057 2M0049B08
C 712	9.2	48.4	30	11	AZ804486	AZ804486 2M0065D07	C 785	9	47.4	19	11	AZ798986	AZ798986 2M0057C12
C 713	9.2	48.4	30	13	CZ476117	CZ476117 d08201-3p	C 786	9	47.4	19	11	AZ799886	AZ799886 2M0060M21
C 714	9.2	48.4	30	13	CZ909411	CZ909411 4018009C0	C 787	9	47.4	19	11	AZ808113	AZ808113 2M0071A01
C 715	9.2	48.4	30	14	AB082245	AB082245 Drosophil	C 788	9	47.4	19	11	AZ820788	AZ820788 2M0093A16
C 716	9.2	48.4	30	14	CR359171	CR359171 Arabidops	C 789	9	47.4	19	11	AZ843215	AZ843215 2M0142B06
C 717	9	47.4	11	1	AJ648107	AJ648107 AJ648107	C 790	9	47.4	19	11	AZ845178	AZ845178 2M0144P16
C 718	9	47.4	17	9	DN986658	DN986658 MSU_28R_2	C 791	9	47.4	19	11	AZ845178	AZ845178 2M0150L21
C 719	9	47.4	17	14	AJ599163	AJ599163 Arabidops	C 792	9	47.4	19	11	AZ849133	AZ849133 2M0150L21
C 720	9	47.4	19	1	AA911671	AA911671 o149f08.s	C 793	9	47.4	19	11	AZ854647	AZ854647 2M0158P15
C 721	9	47.4	19	1	A1142547	A1142547 qb47D08.x	C 794	9	47.4	19	11	AZ861541	AZ861541 2M0168F19
C 722	9	47.4	19	1	A1471695	A1471695 t199f04.x	C 795	9	47.4	19	11	AZ941561	AZ941561 2M0201B19
C 723	9	47.4	19	1	A1683556	A1683556 tx67R08.x	C 796	9	47.4	19	11	AZ969354	AZ969354 2M0242A07
C 724	9	47.4	19	1	A1718147	A1718147 ab42f11.x	C 797	9	47.4	19	13	CL665369	CL665369 PR10149C-
C 725	9	47.4	19	1	AJ7659543	AJ7659543 AJ659543	C 798	9	47.4	20	5	CF279207	CF279207 14ETL--05
C 726	9	47.4	19	1	AJ747090	AJ747090 AJ747090	C 799	9	47.4	20	5	CF302797	CF302797 7LEAF--08
C 727	9	47.4	19	1	AM075425	AM075425 AM075425	C 800	9	47.4	20	5	CF309954	CF309954 ABF--04-F
C 728	9	47.4	19	1	CA794263	CA794263 Cdc_BI_12	C 801	9	47.4	20	5	CF311285	CF311285 ABF--06-H
C 729	9	47.4	19	5	CF280692	CF280692 14ETL--07	C 802	9	47.4	20	5	CF312611	CF312611 ABF--08-H
C 730	9	47.4	19	5	CF282249	CF282249 14ETL--09	C 803	9	47.4	20	5	CF317375	CF317375 HD--07-A1
C 731	9	47.4	19	5	CF295184	CF295184 3ODGS--05	C 804	9	47.4	20	5	CF337475	CF337475 JMT--07-0
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C 734	9	47.4	19	5	CF334492	CF334492 NAEL--07-	C 807	9	47.4	20	9	DR074183	DR074183 ik53a10.g
C 735	9	47.4	19	8	CFX007735	CFX007735 i30b001.g	C 808	9	47.4	20	11	AZ328703	AZ328703 1M0052A07
C 736	9	47.4	19	9	DN953961	DN953961 it66h10.g	C 809	9	47.4	20	11	AZ335199	AZ335199 1M0064K22
C 737	9	47.4	19	9	DR062674	DR062674 iq20d11.g	C 810	9	47.4	20	11	AZ342269	AZ342269 1M0075F13
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C 740	9	47.4	19	11	AZ305212	AZ305212 1M0005I15	C 813	9	47.4	20	11	AZ360709	AZ360709 1M0104N05
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ALIGNMENTS

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ACCESSION     AZ393146
VERSION       AZ393146.1 GI:10508218
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 28)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0156 row: 0 column: 04
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              High quality sequence stop: 28.
FEATURES      Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGClM library"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gil4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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ORIGIN

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Query Match      81.1%; Score 15.4; DB 11; Length 28;
Best Local Similarity 94.1%; Pred. No. 5.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      4  GGAGAGGGGGTGGGTG 20
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RESULT 2

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ACCESSION     AZ307952
VERSION       AZ307952.1 GI:10347459
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
              Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 22)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
COMMENT       University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0010 row: L column: 24
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              High quality sequence stop: 22.
FEATURES      Location/Qualifiers
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/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 70.5%; Score 13.4; DB 11; Length 22;
Best Local Similarity 93.3%; Pred. No. 3.5e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGG 15
|||||
DB 4 CGAGAGGGGGGTGGG 18
|||||

RESULT 3
A1673793
LOCUS
DEFINITION
to73c10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2183922 3,
similar to TR:O65375 O65375 F12F1.9 PROTEIN. ;contains element
MER22 repetitive element ;, mRNA sequence.
ACCESSION
A1673793
VERSION
A1673793.1 GI:4853524
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 22)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1546 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
source
1. .22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2183922"
/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"
/lab_host="DH10B"
/clone_lib="NCI CGAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 Kb. Life Technologies catalog #:
11549-011"

ORIGIN
Query Match 69.5%; Score 13.2; DB 1; Length 22;
Best Local Similarity 83.3%; Pred. No. 4.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAGGGGGTGGGTGCT 19
|||||
DB 1 GAGGAGGGGGGGGTGT 18
|||||

RESULT 4
A1586975
LOCUS
DEFINITION
tw15q05.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259800 3,
similar to SW:EXTN_TOBAC F13983 EXTENSIN PRECURSOR ;, mRNA
sequence.
ACCESSION
A1586975
VERSION
A1586975.1 GI:4573416
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
unknown library type
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2259800"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn52"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; This library represents the normalized
version of NCI CGAP Brn35. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."

ORIGIN
Query Match 67.4%; Score 12.8; DB 1; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGGTG 17
|||||

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Db      3  GGGGAAGGGGGGGGNG 19

RESULT 5
BQ590098
LOCUS
DEFINITION
  E012843-024-019-019-T7 MP12-ADIS-024-storage root Beta vulgaris
ACCESSION
  BQ590098
VERSION
  BQ590098.1  GI:26119681
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 29)
  Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
  12472698
  Contact: Weisshaar B
  ADIS DNA core facility at MPIZ
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weisshaar@mpiz-koeln.mpg.de
  Insert Length: 29 Std Error: 0.00
  Inert: 19 row: 0 column: 19
  Seq primer: T7; GTAATACGACTCATATAGGC.
FEATURES
  source
    1..29
    Location/Qualifiers
      /organism="Beta vulgaris"
      /mol_type="mRNA"
      /cultivar="KWS2320 (double haploid, monogerm breeding
      line)"
      /db_xref="GABI:190019"
      /db_xref="taxon:161934"
      /clone="024-019-019"
      /tissue_type="storage root"
      /lab_host="EMDH10B"
      /clone_lib="MP12-ADIS-024-storage root"
      /note="Vector: PCWVSFOR6; Site 1: Sali; Site 2: NotI;
      cDNA library from sugar beet, library provided by KWS
      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
      b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
      orientation:
      SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
      Sequencing granted in the context of the GABI-Beet
      project, local PI: Dr. Katharina Schneider, coordinator:
      Prof. Christian Jung; Sequence submission managed by
      rzpd/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
  Query Match      67.4%; Score 12.8; DB 3; Length 29;
  Best Local Similarity 87.5%; Pred. No. 6.3e+05;
  Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GAGAGGGGGGGGGTGG 17
      |||||
Db      13  GAGAGGGGGGGGGGG 28

RESULT 6
A2479594
LOCUS
DEFINITION
  IM0300822F Mouse 10kb plasmid UUGClM library Mus musculus genomic
  clone UUGClM0300822 F, genomic survey sequence.
ACCESSION
  A2479594
VERSION
  A2479594.1  GI:10639102

GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
  1 (bases 1 to 22)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: dunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0300 row: B column: 22
  Seq primer: CGTTGTAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 22.
FEATURES
  source
    1..22
    Location/Qualifiers
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGClM0300B22"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGClM library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."
ORIGIN
  Query Match      66.3%; Score 12.6; DB 11; Length 22;
  Best Local Similarity 78.9%; Pred. No. 7.6e+05;
  Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GGAGAAGGGGGGTGGTGCT 19
      |||||
Db      3  GGGTAATGTGGTGGTGCT 21

RESULT 7
A2345548/c
LOCUS
DEFINITION
  1M0080D13F Mouse 10kb plasmid UUGClM library Mus musculus genomic
  clone UUGClM0080D13 F, genomic survey sequence.
ACCESSION
  A2345548

```

```

VERSION AZ345548.1 GI:10424785
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: D column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 65.3%; Score 12.4; DB 11; Length 20;
Best Local Similarity 92.9%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGGTGGG 15
|||||
DB 19 GAGAGGGGGGTGG 6

RESULT 8
AZ486450 24 bp DNA linear GSS 05-OCT-2000
LOCUS IM0314A06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0314A06 R, genomic survey sequence.

```

```

ACCESSION AZ486450
VERSION AZ486450.1 GI:10653235
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0314 row: A column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0314A06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 65.3%; Score 12.4; DB 11; Length 24;
Best Local Similarity 92.9%; Pred. No. 9.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGGTGGG 15
|||||
DB 4 GAGAGGGGGGTGGG 17

RESULT 9
AI000026 22 bp mRNA linear EST 05-JUN-1998
LOCUS AI000026
DEFINITION ot03d12.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613783 3'

```


similar to TR:092853 092853 HU-K4. ;, mRNA sequence.

ACCESSION A1000026
 VERSION A1000026.1 GI:3190580
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 22)
 REFERENCE
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-xemail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio1.llnl.gov/bbrp/image/image.html

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0045 row: J column: 09 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 22. Location/Qualifiers 1. .22
FEATURES	
SOURCE	

ORIGIN

Query Match	64.2%	Score 12.2;	DB 11;	Length 22;
Best Local Similarity	82.4%	Pred. No. 1.1e+05;		
Matches	14.	Mismatches	3.	Gaps 0;
	Conservative			Indels 0;

TITLE Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0057 row: I column: 22
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES

source

1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0057122"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 23;
 Best Local Similarity 82.4%; Pred. No. 1.1e+06;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGGGTGGGTGCT 19
 |||||
 DB 1 AGGAGGGGGTGGAGCT 17

RESULT 12

AZ943422/c
 LOCUS AZ943422 25 bp DNA linear GSS 26-APR-2001
 DEFINITION ZMO204P06F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0204P06 F, genomic survey sequence.

ACCESSION AZ943422
 VERSION AZ943422.1 GI:13807481

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0204 row: P column: 06
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

source

1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0204P06"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 25;
 Best Local Similarity 82.4%; Pred. No. 1.1e+06;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGTG 17
 |||||
 DB 23 GGGGAAGGGGGGGGGG 7

RESULT 13

AZ362697
 LOCUS AZ362697 26 bp DNA linear GSS 02-OCT-2000
 DEFINITION IM0107G23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0107G23 R, genomic survey sequence.

ACCESSION AZ362697
 VERSION AZ362697.1 GI:10476397

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: G column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source
Location/Qualifiers

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0107G23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17

Db 8 GGGGGTGGGGGGTGGGTG 24

RESULT 14

AZ836891
LOCUS 2M0131N22R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0131N22 R, genomic survey sequence.
ACCESSION AZ836891
VERSION AZ836891.1 GI:13006799
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchoontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0131 row: N column: 22
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source
Location/Qualifiers

1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0131N22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17

Db 11 GGAGACGGGGGGGGGGG 27

RESULT 15

AI785472/c
LOCUS AI785472 28 bp mRNA linear EST 02-JUL-1999
DEFINITION uJ42f07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1922629 3' similar to SW:RLX1_HUMAN P49406 PUTATIVE 60S
RIBOSOMAL PROTEIN. ;, mRNA sequence.
ACCESSION AI785472
VERSION AI785472.1 GI:5333188
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchoontoglires; Glires; Rodentia;

REFERENCE
AUTHORS

Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other ESTs: u342f07.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:978921

TITLE
JOURNAL
COMMENT

Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1922629"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DralII
(CACCAGTGTG); Site 2: DralII (CACCAGTGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCAGTGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTTAAAGTGTGG and 3' end
primer GCACCTGCAGTCGACACA."

FEATURES
source

ORIGIN

Query Match 64.2%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGTG 17
|||||
Db 23 GGAGAAGGGGTGGATG 7

RESULT 16
AZ483923/c
LOCUS
DEFINITION
1M0309A22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0309A22 R, genomic survey sequence.

ACCESSION
AZ483923
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

us-10-604-926a-4539.szlm30.rst

REFERENCE
AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0309 row: A column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0309A22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGTG 17
|||||
Db 21 GGCGAAGGGGGGGGGG 5

RESULT 17
AZ274078/c
LOCUS
DEFINITION
2M0003001F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0003001 F, genomic survey sequence.

ACCESSION
AZ274078
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 28)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: 0 column: 01
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0003001"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 64.2%; Score 12.2; DB 11; Length 28;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17
|||||
Db 18 GGAGAGGGGGGGGGGG 2

RESULT 18
AZ642459/c
LOCUS AZ642459 29 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0505D06R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0505D06 R, genomic survey sequence.
ACCESSION AZ642459
VERSION AZ642459.1 GI:11769087
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0505 row: D column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0505D06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 64.2%; Score 12.2; DB 11; Length 29;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17
|||||
Db 23 GGGGAGGGGGGGGGGG 7

RESULT 19
AZ361601
LOCUS AZ361601 30 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0108E01R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0108E01 R, genomic survey sequence.
ACCESSION AZ361601
VERSION AZ361601.1 GI:10475397
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Glires; Rodentia;

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: E column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.

FEATURES
source

1..30
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0106E01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 64.2%; Score 12.2; DB 11; Length 30;
Best Local Similarity 82.4%; Pred. No. 1.1e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGAGGAGGGGGTGGGTG 17
DB 3 GAAGCAGGGGGTGGGGG 19

RESULT 20
AZ405596
LOCUS
DEFINITION
IM0174B06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0174B06 R, genomic survey sequence.
ACCESSION
AZ405596
VERSION
AZ405596.1 GI:10529609
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0174 row: B column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source

1..20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0174B06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 20;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAGGAGGGGGTGGG 15
DB 2 GGGGGAGGGGGTGGG 16

RESULT 21
AZ445481/c
LOCUS
DEFINITION
IM0241P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0241P15 F, genomic survey sequence.
ACCESSION
AZ445481
VERSION
AZ445481.1 GI:10595346
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: P column: 15
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0241P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGG 15
|||||
Db 17 GGATATGGGGTGGG 3

RESULT 22 AZ816100/c

LOCUS AZ816100 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0084M11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0084M11 R, genomic survey sequence.

ACCESSION AZ816100
VERSION AZ816100.1 GI:12986008
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0084 row: M column: 11
Seq primer: CACACGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0084M11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAGGGGGTGGTGCT 19
|||||
Db 21 AAGTGGGTGGGGCT 7

RESULT 23 AZ834089/c

LOCUS AZ834089 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0116C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0116C12 R, genomic survey sequence.

ACCESSION AZ834089
VERSION AZ834089.1 GI:13003997
KEYWORDS GSS.

SOURCE
ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0116 row: C column: 12
 Seq primer: CACACGAGAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.
FEATURES
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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UUGC2M0116C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 62.1%; Score 11.8; DB 11; Length 21;
 Best Local Similarity 86.7%; Pred. No. 1.6e+06;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GGAGAAAGGGGGTGGG 15
 |||||
 Db 16 GGGGAAGGGGGGGG 2

RESULT 24
 BH000494
 LOCUS 2M0288H21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0288H21 F, genomic survey sequence.
 ACCESSION BH000494
 VERSION BH000494.1 GI:13871720

KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0288 row: H column: 21
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0288H21"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 62.1%; Score 11.8; DB 11; Length 24;
 Best Local Similarity 86.7%; Pred. No. 1.6e+06;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GGAGAAAGGGGGTGGG 15
 |||||
 Db 10 GGAGAGGGGGGGGGG 24

RESULT 25
 AA878831
 LOCUS 25 bp mRNA linear EST 25-MAR-1998
 DEFINITION of83f10.s1 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1436971 3'
 similar to TR:Q43687 Q43687 EXTENSIN-LIKE PROTEIN ;contains MSRI.b1
 TARI repetitive element ;, mRNA sequence.


```

ACCESSION      AA878831
VERSION        AA878831.1  GI:2987796
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgapbs-r@mail.nih.gov
               unknown library type
               Trace considered overall poor quality
               Seq primer: -40m13 fwd. ET from Amersham
               High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..25
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               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:1436971"
               /tissue_type="hepatic adenoma"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP L15"
               /note="Organ: liver; Vector: pCMV-SPORT4; Site:1: Salt;
               Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 0.8 kb."
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGAGAGGGGGTGGG 15
Db 3 CGAGAGGGGGTGGG 17

RESULT 26
LOCUS      AI628239
DEFINITION ty93c04.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286630 3'
           similar to TR:Q01944 Q01944 EXTENSIN ;contains element MSR1
           repetitive element ;, mRNA sequence.
ACCESSION  AI628239
VERSION     AI628239.1  GI:4665039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE   1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Trace considered overall poor quality

ACCESSION      AA878831
VERSION        AA878831.1  GI:2987796
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE      1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgapbs-r@mail.nih.gov
               unknown library type
               Trace considered overall poor quality
               Seq primer: -40m13 fwd. ET from Amersham
               High quality sequence stop: 1.
FEATURES       Location/Qualifiers
               1..25
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
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               /tissue_type="hepatic adenoma"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP L15"
               /note="Organ: liver; Vector: pCMV-SPORT4; Site:1: Salt;
               Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 0.8 kb."
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGAGAGGGGGTGGG 15
Db 3 CGAGAGGGGGTGGG 17

RESULT 26
LOCUS      AI628239
DEFINITION ty93c04.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2286630 3'
           similar to TR:Q01944 Q01944 EXTENSIN ;contains element MSR1
           repetitive element ;, mRNA sequence.
ACCESSION  AI628239
VERSION     AI628239.1  GI:4665039
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE   1 (bases 1 to 25)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Trace considered overall poor quality

Insert Length: 1021 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
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               /clone="IMAGE:2286630"
               /tissue_type="well-differentiated endometrial
               adenocarcinoma, 7 pooled tumors"
               /lab_host="DH10B"
               /clone_lib="NCI CGAP Utl"
               /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
               Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
               Average insert size 1.75 Kb. Life Technologies catalog #:
               11538-014"
ORIGIN
Query Match      62.1%; Score 11.8; DB 1; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTG 17
Db 1 AGAAGGGGGGGGGG 15

RESULT 27
LOCUS      AZ391369
DEFINITION clone UUGC1M0153K24 F, genomic survey sequence.
ACCESSION  AZ391369
VERSION     AZ391369.1  GI:10506412
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 25)
               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
               Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
               Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
               Niederhausern, A. and Wright, D., Weiss, R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
JOURNAL        Contact: Robert B. Weiss
COMMENT        University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: dunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Seq primer: CGTTGTAACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 25.
FEATURES       Location/Qualifiers
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               /organism="Mus musculus"
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               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0153K24"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"

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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGG 15
|||||
Db 8 GGAGAGGGGGGGGG 22

RESULT 28

AZ772979

LOCUS

DEFINITION 1M0584E13F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0584E13 F, genomic survey sequence.

ACCESSION

AZ772979

VERSION

AZ772979.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

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University of Utah

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0584 row: E column: 13

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

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/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUC1M0584E13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 25;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGGTG 17
|||||
Db 3 AAAGGGGAGTGGGTG 17

RESULT 29

AZ843200

LOCUS

DEFINITION 2M0141024R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC2M0141024 R, genomic survey sequence.

ACCESSION

AZ843200

VERSION

AZ843200.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 26)

Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0141 row: O column: 24

Seq primer: CACACAGGAACAGGTATGACC

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1..26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUC2M0141024"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 26;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTG 17
| | | | | | | | | |
Db 1 AAAAGGAGTGGGTG 15

RESULT 30

AZ477874/c
LOCUS
DEFINITION
28 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0297022 F, genomic survey sequence.

ACCESSION
AZ477874
VERSION
GSS.

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0297 row: 0 column: 22

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0297022"

FEATURES

source

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 62.1%; Score 11.8; DB 11; Length 28;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGGTG 17
| | | | | | | | | |
Db 19 ATAAGGGGTGGGTG 5

RESULT 31

AZ489682

LOCUS

DEFINITION

28 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0322G16 F, genomic survey sequence.

ACCESSION
AZ489682
VERSION
GSS.

KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0322 row: G column: 16

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

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/clone="UUGC1M0322G16"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 11; Length 28;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGTG 17
DB 7 AGAAGTGGGGGGT 21

RESULT 32
LOCUS CX012159 29 bp mRNA linear EST 06-DEC-2004
DEFINITION io57g07.b1 Whole Heart Library (DOGEST5) Canis familiaris cDNA, mRNA sequence.
ACCESSION CX012159.1 GI:56394570
VERSION CX012159.1
KEYWORDS EST:
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 29)
AUTHORS Balija,V.S., Nascimento,L.U. and McCombie,W.R.
TITLES ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Auenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Location/Qualifiers
1..29
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGEST5)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street,

/clone="UUGC1M0322G16"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/sex="Male"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 62.1%; Score 11.8; DB 8; Length 29;
Best Local Similarity 86.7%; Pred. No. 1.6e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTG 16
DB 11 GTGCAGGGGGTGGGT 25

RESULT 33
LOCUS AI758492 22 bp mRNA linear EST 16-DEC-1999
DEFINITION ty08d06.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278475 3', similar to TR:048803 O48809 F24O1.18.;, mRNA sequence.
ACCESSION AI758492
VERSION AI758492.1 GI:5152215
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 22)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 736 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2278475"
/tissue_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI-CGAP Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

ORIGIN
Query Match 61.1%; Score 11.6; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGTGC 18
DB 21 GCGCAGGGGGGGGGGGC 4

RESULT 34
LOCUS AZ627855 24 bp DNA linear GSS 13-DEC-2000

```

DEFINITION 1M0476C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0476C06 F, genomic survey sequence.

ACCESSION AZ627855

VERSION AZ627855.1 GI:11750141

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: C column: 06
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

source
1..24
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0476C06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.1%; Score 11.6; DB 11; Length 24;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGGTGGGTGC 18
||| ||||| ||||| |||||

Db 3 GGGAAAAGGGGTGGGTTC 20

RESULT 35
CZ915711/c

LOCUS CZ915711 27 bp DNA linear GSS 08-AUG-2005

DEFINITION 4013012G12.2BL.x1.4013 - RescueMu Grid O Zea mays genomic survey sequence.

ACCESSION CZ915711

VERSION CZ915711.1 GI:71933250

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 27)

Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013012 row: G column: 12
Class: transposon-tagged.

FEATURES

source
1..27
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 61.1%; Score 11.6; DB 13; Length 27;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGGTGGGTGC 18
||| ||||| ||||| |||||

Db 18 GGGGAGGGGGGGGGGGGC 1

RESULT 36
BM396069

LOCUS BM396069 29 bp mRNA linear EST 17-JAN-2002

DEFINITION 5009-0-16-F06.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396069

VERSION BM396069.1 GI:18196122

KEYWORDS EST.

ORGANISM

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 29)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

```

TITLE      Frankel, J. and Klobutcher, L.
JOURNAL    EST from Tetrahymena thermophila, strain CU428.1, growing cells
COMMENT    Unpublished (2002)

Contact:  Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES   Location/Qualifiers
            1..29
             /organism="Tetrahymena thermophila"
             /mol_type="mRNA"
             /strain="CU428.1"
             /db_xref="taxon:5911"
             /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
             /note="Vector: BlueScript2 SK+; Details on library
             preparation can be found in Chilcoat and Turkewitz (2001).
             Proc. Natl. Acad. Sci. USA. 98: 8709-8713."

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	Query Match	61.1%;	Score 11.6;	DB 2;	Length 29;
	Best Local Similarity	77.8%;	Pred. No. 2e+06;		
	Matches 14;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	GGAGAGGCGGTGGTGTC	18	*	
Db	6	GGAGCTCCGGTGGTGTC	23		

RESULT	37
AZ853274/c	
LOCUS	
DEFINITION	AZ853274 linear DNA 30 bp GSS 21-FEB-2001 M0156D23F Mouse 10kb plasmid UGCDIM library Mus musculus genomic clone UGC2M0156D23 F, genomic survey sequence.
ACCESSION	AZ853274
VERSION	AZ853274.1 GI:13041223
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 30) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: D column: 23
Seq primer: CGTGTAAACGAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="BTGC2M0156D23"

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`/sex="Male"`
`/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"`
`/clone_lib="Mouse 10kb plasmid UUGC1M library"`
`/notes="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."`

ORIGIN

```

Query Match          61.1%; Score 11.6; DB 11; Length 30;
Best Local Similarity 77.8%; Pred. No. 28+06;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      .      1  GGAGAGAGGGGTGGGTGC 18
          ||| ||| ||| ||| ||| |||
Db       18  GGGGAGAGGGGGGGGGGC 1

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RESULT 38	13 bp	linear	EST 06-NOV-2001
LOCUS	13 bp	mrna	
DEFINITION	HN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
ACCESSION	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
VERSION	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
KEYWORDS	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
SOURCE	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
ORGANISM	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
REFERENCE	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
AUTHORS	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
TITLE	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
JOURNAL	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
PUBLISHED	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	
COMMENT	BN23-1-E8.R HNC (Human Normal Cartilage)	EST 06-NOV-2001	

UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7
Location/Qualifiers
1. .13 .
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN		and selected for ampicillin resistance."	
Query Match		60.0%;	Score 11.4; DB 2; Length 13;
Best Local Similarity		92.3%;	Pred. No. 2.4e+06;
Matches		12; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy		1	GGAGAAGGGGGTG 13
Db		13	GGAGAAGGGGGAG 1
RESULT 39			
A2787717			
LOCUS		A2787717 19 bp DNA linear GSS 16-FEB-2001	
DEFINITION		2M0034A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034A21 F, genomic survey sequence.	
ACCESSION		A2787717	
VERSION		GSS	
KEYWORDS		Mus musculus (house mouse)	
SOURCE		Mus musculus	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.	
REFERENCE		1 (bases 1 to 19)	
AUTHORS		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.	
TITLE		Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 row: A column: 21 Seq primer: CGTTGTAAACACGCCACGT Class: plasmid ends High quality sequence stop: 19.	
FEATURES		Location/Qualifiers	
source		1..19	
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		/mol_type="genomic DNA"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/clone="UUGC2M0034A21"	
		/sex="Male"	
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: pWD42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells	
ORIGIN			
Query Match		60.0%;	Score 11.4; DB 1; Length 22;
Best Local Similarity		92.3%;	Pred. No. 2.4e+06;
Matches		12; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy		5	AAGGGGGTGGGTG 17
Db		21	AAGGGGGGGGGTG 9
RESULT 41			
A2351959			
LOCUS		A2351959 22 bp DNA linear GSS 29-SEP-2000	
DEFINITION		1M0090C16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0090C16 F, genomic survey sequence.	
ACCESSION		A2351959	
ORIGIN			
Query Match		60.0%;	Score 11.4; DB 1; Length 22;
Best Local Similarity		92.3%;	Pred. No. 2.4e+06;
Matches		12; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy		5	AAGGGGGTGGGTG 17
Db		21	AAGGGGGGGGGTG 9
RESULT 41			
A2351959			
LOCUS		A2351959 22 bp DNA linear GSS 29-SEP-2000	
DEFINITION		1M0090C16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0090C16 F, genomic survey sequence.	
ACCESSION		A2351959	

```

VERSION AZ351959.1 GI:10431196
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0090 row: C column: 16
Seq primer: CCGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0090C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 60.0%; Score 11.4; DB 11; Length 22;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AAGGGGGTGGGTG 17
DB 6 ATGGGGGTGGGTG 18

RESULT 42
AZ404383 23 bp DNA linear GSS 03-OCT-2000
LOCUS IM0172119R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0172119 R, genomic survey sequence.

ACCESSION AZ404383
VERSION AZ404383.1 GI:10528492
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: I column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
source
1..23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0172119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 60.0%; Score 11.4; DB 11; Length 23;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGGGGTGGGTGCT 19
DB 1 GGGGGTGGGTGCT 13

RESULT 43
AZ404383 25 bp mRNA linear EST 31-JUL-1998
LOCUS AI066777
DEFINITION ovi7a05.x1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1637552 3'

```



```

similar to TR:Q39599 Q39599 EXTENSIN. ; contains MSR1.t2 MSRI
repetitive element ;, mRNA sequence.
ACCESSION AI066777.1 GI:3367063
VERSION AI066777.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 25)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40m13 fwd. Et from AmerSham
High quality sequence stop: 1.
FEATURES
    source
        1..25
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1637552"
            /tissue_type="pooled germ cell tumors"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP GC3"
            /note="Vector: pRT3D-PacI; 1st strand cDNA was prepared
            from 3 pooled germ cell tumors, and was then primed with a
            Not I - oligo(dT) primer. Double-stranded cDNA was ligated
            to Eco RI adaptors (Pharmacia), digested with Not I and
            cloned into the Not I and Eco RI sites of the modified
            pRT3 vector. Library is not normalized. Library was
            constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
    Query Match 60.0%; Score 11.4; DB 1; Length 25;
    Best Local Similarity 92.3%; Pred. No. 2.4e+06;
    Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 AGAAGGGGGTGGG 15
Db 13 AAAAGGGGGTGGG 1
RESULT 44
LOCUS DU777397 27 bp DNA linear GSS 27-JAN-2006
DEFINITION ASXB1637.b2 HF500_10-06-02 uncultured marine microorganism
HF500_10-06-02 genomic clone HF0500_077E01, genomic survey
sequence.
ACCESSION DU777397
VERSION DU777397.1 GI:85791593
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF500_10-06-02
ORGANISM uncultured marine microorganism HF500_10-06-02
unclassified sequences; environmental samples.
1 (bases 1 to 27)
REFERENCE DeLong,E.F., Presnott,C.M., Mincer,T., Rich,V., Hallam,S.J.,
Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
and Karl,D.M.
Comparative genomics reveals ecological trends in stratified

```

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microbial communities in the ocean's interior
Science (2006) In press
Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,
Kerrie Barry, Rijana Glavinadelrio, David Bruce, Paul Richardson
and Edward DeLong
US DOE Joint Genome Institute
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
Tel: 617-253-5271
Fax: 617-253-2679
Email: PMRichardson@lbl.gov; delong@mit.edu
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
DNA library prepared from marine picoplankton in the less than 1.6
um, greater than 0.22 um fraction. Sample Date: 10/6/2002
Coordinates: 22.45 N, 158 W Depth 500 m Temperature: 7.25 C
Salinity: 34.07 psu Oxygen: 118.0 umol/kg
Class: fosmid ends.
FEATURES
    source
        1..27
            /organism="uncultured marine microorganism HF500_10-06-02"
            /mol_type="genomic DNA"
            /db_xref="taxon:361149"
            /clones="HF0500_077E01"
            /cell_type="marine picoplankton, less than 1.8 um, greater
            than 0.22 um fraction"
            /clone_lib="HF500_10-06-02"
            /note="Vector: pCC1FOS; North Pacific Subtropical Gyre
            (Hawaii) picoplankton genomic fosmid DNA library prepared
            from marine picoplankton in the less than 1.6 um, greater
            than 0.22 um fraction. Picoplankton collected at 500 m
            depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample
            Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 500 m
            Temperature: 7.25 C Salinity: 34.07 psu Oxygen: 118.0
            umol/kg"
ORIGIN
    Query Match 60.0%; Score 11.4; DB 14; Length 27;
    Best Local Similarity 85.7%; Pred. No. 2.4e+06;
    Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAGAGGGGGTGG 14
Db 13 GGAGAGGGGGGGG 26
RESULT 45
AI567156/c
LOCUS AI567156 28 bp mRNA linear EST 13-MAY-1999
DEFINITION tp50b06.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2191187 3'
similar to TR:Q39600 Q39600 EXTENSIN. ;, mRNA sequence.
ACCESSION AI567156
VERSION AI567156.1 GI:4525608
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 28)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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Trace considered overall poor quality
Insert length: 2563 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES

source
1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2191187"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.48 Kb. Life technologies catalog #: 11542-016"

ORIGIN

Query Match 60.0%; Score 11.4; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 2.4e+06;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 GGAGAGGGGGTGC 13
||| ||||| |||||
15 GGGGAGGGGGTGC 3

Db

RESULT 46

DN988622

LOCUS

DN988622 20 bp mRNA linear EST 17-MAY-2005
ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1 Bermudagrass line Zebra
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1, mRNA sequence.

ACCESSION

DN988622

VERSION

DN988622.1

KEYWORDS

EST.

SOURCE

Cynodon dactylon (Bermuda grass)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Melmaie, K., Elavarthi, S. and Guenzi, A.C.

TITLE

Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays

JOURNAL

Unpublished (2005)

COMMENT

Contact: Guenzi AC

Dep. of Plant and Soil Sciences

Oklahoma State University

368 Agriculture Hall, Stillwater, OK 74078-6028, USA

Tel: 405-744-6028

Fax: 405-744-6039

Email: acg@mail.pss.okstate.edu

PCR Primers

FORWARD: M13 forward

BACKWARD: M13 Reverse

Seq primer: M13 Forward.

FEATURES

source

1. .20

/organism="Cynodon dactylon"

/mol_type="mRNA"

/cultivar="Zebra"

/db_xref="taxon:28909"

/clone="ZEBRA_28R_2-II_02_ZEBRA_28R_2-II_02_E09.ab1"

/tissue_type="crown"

/lab_host="E. coli"

/clone_lib="Bermudagrass line Zebra subtracted cold
acclimated cDNA library"

ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 2.9e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

3 AGAAGGGGGTGGTGC 18
||| ||||| |||||

Db

5 AAAAGGGGGGGGAGC 20
||| ||||| |||||

RESULT 47

AZ864022

LOCUS

AZ864022 21 bp DNA linear GSS 21-FEB-2001
2M0173G22F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0173G22 F, genomic survey sequence.

ACCESSION

AZ864022

VERSION

AZ864022.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 21)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0173 row: G column: 22

Seq primer: GTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0173G22"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

Qy 3 AGAAGGGGTGGGTGC 18
p/p 2 AGGGGGGGGGGGTGC 17

MUS MUSCULUS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0037 row: M column: 14

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0037M14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.9%; Score 11.2; DB 11; Length 22;

Best Local Similarity 81.2%; Pred. No. 2.9e+06;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGTGGGT 16

DB 3 GGGGAGTGGGTGGGT 18

Search completed: October 14, 2006, 20:50:41

Job time : 2320 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:41:06 ; Search time 100 Seconds
(without alignments) 355.511 Million cell updates

Title: US-10-604-926A-4539

Perfect score: 19
Sequence: 1 qqaaagggggtgggtgct 19

Scoring table: IDENTITY NUC

Scoring cable: IDENTITY_NOC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs. 93554401 residues

Total number of hits satisfying chosen parameters: 1097684

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Minimum DB seq length: 0
Maximum DB seq length: 30
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents NA:*

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Database :
issuere_ratings_vla:
1: /EMC Celerra SDS3/prodata/2/ina/1 COMB.seq:*
2: /EMC Celerra SDS3/prodata/2/ina/5 COMB.seq:*
3: /EMC Celerra SDS3/prodata/2/ina/6A COMB.seq:*
4: /EMC Celerra SDS3/prodata/2/ina/6B COMB.seq:*
5: /EMC Celerra SDS3/prodata/2/ina/7 COMB.seq:*
6: /EMC Celerra SDS3/prodata/2/ina/H COMB.seq:*
7: /EMC Celerra SDS3/prodata/2/ina/FCUS COMB.seq:*
8: /EMC Celerra SDS3/prodata/2/ina/PP COMB.seq:*
9: /EMC Celerra SDS3/prodata/2/ina/RE COMB.seq:*
10: /EMC Celerra SDS3/prodata/2/ina/backfiles1.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
C 1	13.8	72.6	20	3	US-08-914-961-8	Sequence 8, Appli	
C 2	13.4	70.5	22	3	US-10-085-612A-23	Sequence 23, Appli	
C 3	13.2	69.5	18	3	US-09-422-978-9827	Sequence 9827, Ap	
C 4	13.2	69.5	21	3	US-09-792-686A-21	Sequence 21, Appli	
C 5	13.2	69.5	25	3	US-09-067-626-12	Sequence 12, Appli	
C 6	12.8	67.4	27	2	US-08-173-489C-359	Sequence 359, App	
C 7	12.6	66.3	25	3	US-08-943-731-424	Sequence 424, App	
C 8	12.4	65.3	17	3	US-09-282-146-4	Sequence 4, Appli	
C 9	12.4	65.3	18	3	US-09-205-921-33	Sequence 33, Appli	
C 10	12.4	65.3	21	3	US-09-657-472-246	Sequence 246, App	
C 11	12.4	65.3	22	3	US-08-927-219-64	Sequence 64, Appli	
C 12	12.4	65.3	27	3	US-09-716-964B-191	Sequence 191, App	
C 13	12.4	65.3	30	2	US-08-504-511A-6	Sequence 6, Appli	
C 14	12.4	65.3	30	3	US-09-119-507B-8	Sequence 10, Appli	
C 15	12.4	65.3	30	3	US-09-119-507B-38	Sequence 38, Appli	
C 16	12.4	65.3	30	3	US-09-119-507B-39	Sequence 39, Appli	
C 17	12.4	65.3	30	3	US-08-897-556A-10	Sequence 10, Appli	
C 18	12.4	65.3	30	3	US-08-897-556A-38	Sequence 38, Appli	
C 19	12.4	65.3	30	3	US-08-897-556A-39	Sequence 39, Appli	
C 20	12.4	65.3	30	3	US-09-547-693-10	Sequence 10, Appli	
C 21	12.4	65.3	30	3	US-09-547-693-38	Sequence 38, Appli	
C 22	12.4	65.3	30	3	US-09-547-693-39	Sequence 39, Appli	
C 23	12.2	64.2	18	2	US-08-531-555-122	Sequence 122, App	

97	11.8	62.1	28	3	US-08-442-144A-74	Sequence 74, Appl	170	11.2	58.9	22	2	US-08-753-979A-24	Sequence 24, Appl
98	11.8	62.1	28	3	US-08-441-970-74	Sequence 74, Appl	171	11.2	58.9	22	2	US-08-753-979A-40	Sequence 40, Appl
99	11.6	61.1	30	3	US-09-735-271-1614	Sequence 1614, Ap	c 172	11.2	58.9	22	3	US-09-305-384-A	Sequence 4, Appl
100	11.6	61.1	18	5	US-10-006-069A-117	Sequence 117, App	c 173	11.2	58.9	22	4	US-09-441-857-42	Sequence 42, Appl
c 101	11.6	61.1	19	3	US-09-913-524-28	Sequence 28, Appl	174	11.2	58.9	23	3	US-09-167-681-10	Sequence 10, Appl
c 102	11.6	61.1	19	3	US-09-632-748-5	Sequence 5, Appl	175	11.2	58.9	23	3	US-09-851-896-6	Sequence 6, Appl
c 103	11.6	61.1	19	3	US-09-332-803A-44	Sequence 44, Appl	176	11.2	58.9	23	3	US-09-778-898A-2	Sequence 2, Appl
c 104	11.6	61.1	19	3	US-09-573-740A-25	Sequence 25, Appl	177	11.2	58.9	23	3	US-09-778-898A-6	Sequence 6, Appl
c 105	11.6	61.1	20	2	US-09-117-952-424	Sequence 424, App	178	11.2	58.9	24	2	US-07-832-905B-72	Sequence 72, Appl
c 106	11.6	61.1	20	3	US-09-522-775A-6	Sequence 6, Appl	c 179	11.2	58.9	24	2	US-08-598-591-18	Sequence 18, Appl
c 107	11.6	61.1	20	3	US-08-836-734E-43	Sequence 43, Appl	c 180	11.2	58.9	24	2	US-08-798-691-22	Sequence 22, Appl
c 108	11.6	61.1	20	3	US-09-906-158-34	Sequence 34, Appl	181	11.2	58.9	24	2	US-08-700-757-72	Sequence 72, Appl
c 109	11.6	61.1	24	3	US-09-820-182-9	Sequence 9, Appl	c 182	11.2	58.9	24	2	US-08-480-640A-127	Sequence 127, App
c 110	11.6	61.1	25	3	US-08-818-581B-2	Sequence 2, Appl	c 183	11.2	58.9	24	3	US-08-825-487A-22	Sequence 22, Appl
c 111	11.6	61.1	25	3	US-09-396-196G-115987	Sequence 115987,	c 184	11.2	58.9	24	3	US-08-295-802-127	Sequence 22, Appl
c 112	11.6	61.1	27	3	US-09-940-244-310	Sequence 310, App	c 185	11.2	58.9	24	3	US-09-074-476-22	Sequence 22, Appl
c 113	11.6	61.1	27	3	US-09-777-430C-40	Sequence 40, Appl	c 186	11.2	58.9	24	3	US-08-488-237A-127	Sequence 127, App
c 114	11.6	61.1	30	2	US-08-123-702-26	Sequence 26, Appl	c 187	11.2	58.9	24	3	US-08-375-992A-127	Sequence 127, App
c 115	11.4	60.0	14	3	US-09-808-457-10	Sequence 10, Appl	188	11.2	58.9	24	3	US-09-123-728-3	Sequence 3, Appl
c 116	11.4	60.0	17	3	US-09-360-416-6	Sequence 6, Appl	c 189	11.2	58.9	24	3	US-08-472-679H-127	Sequence 127, App
c 117	11.4	60.0	17	3	US-10-175-225-6	Sequence 6, Appl	c 190	11.2	58.9	24	3	US-09-734-672A-22	Sequence 22, Appl
c 118	11.4	60.0	20	2	US-08-828-511-16	Sequence 16, Appl	c 191	11.2	58.9	25	2	US-09-923-327A-88	Sequence 88, Appl
c 119	11.4	60.0	20	3	US-09-198-452A-6205	Sequence 6205, Ap	192	11.2	58.9	25	2	US-08-495-743-63	Sequence 63, Appl
c 120	11.4	60.0	20	3	US-09-198-452A-6208	Sequence 6208, Ap	193	11.2	58.9	25	2	US-08-495-739-63	Sequence 63, Appl
c 121	11.4	60.0	20	3	US-09-904-420A-8	Sequence 8, Appl	194	11.2	58.9	25	2	US-08-495-741-63	Sequence 63, Appl
c 122	11.4	60.0	20	7	PCF-US94-04361-9	Sequence 9, Appl	195	11.2	58.9	25	3	US-08-062-023-63	Sequence 63, Appl
c 123	11.4	60.0	22	3	US-08-891-271-23	Sequence 23, Appl	c 196	11.2	58.9	25	3	US-10-766-190-15	Sequence 15, Appl
c 124	11.4	60.0	22	3	US-09-018-138-15	Sequence 15, Appl	197	11.2	58.9	26	2	US-08-675-828A-63	Sequence 63, Appl
c 125	11.4	60.0	22	3	US-08-890-929-3	Sequence 3, Appl	c 198	11.2	58.9	26	2	US-08-859-998-532	Sequence 532, App
c 126	11.4	60.0	22	3	US-09-959-007-3	Sequence 3, Appl	c 199	11.2	58.9	26	3	US-09-225-928-532	Sequence 532, App
c 127	11.4	60.0	23	3	US-09-149-922-47	Sequence 47, Appl	c 200	11.2	58.9	26	3	US-09-225-201B-532	Sequence 532, App
c 128	11.4	60.0	24	3	US-09-999-833A-239	Sequence 239, App	201	11.2	58.9	27	3	US-09-678-300-21	Sequence 21, Appl
c 129	11.4	60.0	24	3	US-10-020-445A-239	Sequence 239, App	202	11.2	58.9	27	3	US-09-255-518C-30	Sequence 30, Appl
c 130	11.4	60.0	24	4	US-09-978-189-239	Sequence 239, App	c 203	11.2	58.9	27	3	US-09-791-500-28	Sequence 28, Appl
c 131	11.4	60.0	24	4	US-10-017-085A-239	Sequence 239, App	c 204	11.2	58.9	27	3	US-09-619-380-10	Sequence 10, Appl
c 132	11.4	60.0	24	5	US-10-145-129A-239	Sequence 239, App	205	11.2	58.9	27	5	US-09-762-278-13	Sequence 13, Appl
c 133	11.4	60.0	24	5	US-10-013-929A-239	Sequence 239, App	c 206	11.2	58.9	30	2	US-10-655-073-10	Sequence 10, Appl
c 134	11.4	60.0	24	5	US-10-013-917A-239	Sequence 239, App	207	11.2	58.9	30	3	US-08-384-708A-145	Sequence 145, App
c 135	11.4	60.0	26	3	US-09-367-513-8	Sequence 8, Appl	208	11.2	58.9	30	3	US-08-687-421-145	Sequence 145, App
c 136	11.4	60.0	27	3	US-08-948-113D-15	Sequence 15, Appl	209	11.2	58.9	30	3	US-08-442-423-145	Sequence 145, App
c 137	11.4	60.0	27	3	US-08-815-923-19	Sequence 19, Appl	210	11	57.9	11	2	US-08-231-193A-9	Sequence 9, Appl
c 138	11.4	60.0	28	2	US-08-928-692-7	Sequence 7, Appl	211	11	57.9	11	2	US-08-486-273A-9	Sequence 9, Appl
c 139	11.4	60.0	28	3	US-09-339-972-7	Sequence 7, Appl	212	11	57.9	11	3	US-08-480-474-9	Sequence 9, Appl
c 140	11.4	60.0	29	3	US-09-304-232-552	Sequence 552, App	213	11	57.9	11	3	US-08-940-086A-9	Sequence 9, Appl
c 141	11.4	60.0	29	3	US-09-848-537A-24	Sequence 24, Appl	214	11	57.9	11	3	US-08-940-035A-9	Sequence 9, Appl
c 142	11.4	60.0	29	3	US-09-775-743C-30	Sequence 30, Appl	215	11	57.9	11	3	US-08-935-105A-9	Sequence 9, Appl
c 143	11.4	60.0	29	3	US-09-932-812A-1	Sequence 1, Appl	216	11	57.9	11	3	US-09-648-797-9	Sequence 9, Appl
c 144	11.4	60.0	30	3	US-11-016-518A-1	Sequence 41, Appl	217	11	57.9	11	3	US-10-038-937-9	Sequence 9, Appl
c 145	11.4	60.0	30	3	US-09-733-042-41	Sequence 41, Appl	218	11	57.9	11	3	US-10-007-747-9	Sequence 9, Appl
c 146	11.2	58.9	17	5	US-10-156-308B-3651	Sequence 3651, Ap	219	11	57.9	11	3	US-09-945-901-9	Sequence 9, Appl
c 147	11.2	58.9	19	2	US-08-473-096-17	Sequence 17, Appl	220	11	57.9	11	3	US-08-173-489C-261	Sequence 261, App
c 148	11.2	58.9	20	2	US-08-136-811-15	Sequence 15, Appl	221	11	57.9	12	2	US-08-173-489C-253	Sequence 253, App
c 149	11.2	58.9	20	2	US-08-031-147A-49	Sequence 49, Appl	222	11	57.9	13	2	US-08-233-002A-1	Sequence 1, Appl
c 150	11.2	58.9	20	2	US-08-487-141B-82	Sequence 82, Appl	c 223	11	57.9	19	2	US-08-953-230A-1	Sequence 1, Appl
c 151	11.2	58.9	20	2	US-08-487-141B-83	Sequence 83, Appl	c 224	11	57.9	19	3	US-08-224-232A-1	Sequence 1, Appl
c 152	11.2	58.9	20	2	US-08-835-770-15	Sequence 15, Appl	c 225	11	57.9	19	3	US-08-145-826A-1	Sequence 1, Appl
c 153	11.2	58.9	20	2	US-08-628-731-15	Sequence 15, Appl	c 226	11	57.9	19	3	US-09-668-532-1	Sequence 1, Appl
c 154	11.2	58.9	20	2	US-08-927-561-82	Sequence 82, Appl	c 227	11	57.9	19	3	US-09-580-043B-6	Sequence 6, Appl
c 155	11.2	58.9	20	3	US-09-166-186-133	Sequence 133, App	c 228	11	57.9	19	3	US-08-459-713-1	Sequence 1, Appl
c 156	11.2	58.9	20	3	US-09-429-322-56	Sequence 56, Appl	c 229	11	57.9	19	3	US-08-918-407-1	Sequence 1, Appl
c 157	11.2	58.9	20	3	US-09-313-932-133	Sequence 133, App	c 230	11	57.9	19	3	US-09-413-109-1	Sequence 1, Appl
c 158	11.2	58.9	20	3	US-09-422-978-9212	Sequence 9212, Ap	c 231	11	57.9	19	3	US-10-180-895-1	Sequence 1, Appl
c 159	11.2	58.9	20	7	PCF-US94-02471-49	Sequence 49, Appl	c 232	11	57.9	19	3	US-08-626-678-1	Sequence 1, Appl
c 160	11.2	58.9	20	7	PCF-US96-09388-82	Sequence 82, Appl	c 233	11	57.9	19	5	US-10-170-240-1	Sequence 1, Appl
c 161	11.2	58.9	20	7	PCF-US96-09388-82	Sequence 82, Appl	c 234	11	57.9	20	3	US-09-166-186-131	Sequence 131, App
c 162	11.2	58.9	20	7	PCF-US96-09388-82	Sequence 83, Appl	c 235	11	57.9	20	3	US-09-313-932-131	Sequence 21, App
c 163	11.2	58.9	21	2	US-08-440-787A-39	Sequence 39, Appl	c 236	11	57.9	20	3	US-09-721-822A-21	Sequence 21, Appl
c 164	11.2	58.9	21	3	US-08-367-685-39	Sequence 39, Appl	c 237	11	57.9	20	3	US-09-721-822A-22	Sequence 22, Appl
c 165	11.2	58.9	21	3	US-09-109-663-4	Sequence 4, Appl	c 238	11	57.9	20	3	US-09-980-052-89	Sequence 89, Appl
c 166	11.2	58.9	21	3	US-09-657-472-1486	Sequence 1486, Ap	c 239	11	57.9	20	3	US-10-002-623-120	Sequence 120, App
c 167	11.2	58.9	21	7	PCF-US91-07141-39	Sequence 39, Appl	240	11	57.9	20	3	US-10-002-623-120	Sequence 103, App
c 168	11.2	58.9	22	2	US-08-531-556-98	Sequence 98, Appl	241	11	57.9	21	3	US-08-469-318-103	Sequence 103, App
c 169	11.2	58.9	22	2	US-08-753-979A-10	Sequence 10, Appl	242	11	57.9	21	3	US-08-468-609A-103	Sequence 103, App

243	11	57.9	21	3	US-09-311-912-6	Sequence 6, Appli	Sequence 6, Appli	Sequence 5568, Ap
244	11	57.9	21	3	US-08-737-061-4	Sequence 4, Appli	Sequence 74, Appl	
245	11	57.9	21	3	US-08-446-872A-103	Sequence 103, App	Sequence 322, App	
246	11	57.9	21	3	US-08-762-227A-103	Sequence 103, App	Sequence 322, App	
247	11	57.9	21	3	US-09-510-238A-74	Sequence 74, Appl	Sequence 33, Appl	
248	11	57.9	21	3	US-09-158-272-4	Sequence 4, Appli	Sequence 4, Appli	
c 249	11	57.9	21	3	US-09-269-717-8	Sequence 8, Appli	Sequence 27, Appl	
250	11	57.9	21	3	US-08-957-610A-378	Sequence 378, App	Sequence 5, Appli	
251	11	57.9	21	7	PCT-US95-01185-103	Sequence 103, App	Sequence 24, Appl	
c 252	11	57.9	22	2	US-08-332-766A-69	Sequence 69, Appl	Sequence 5, Appli	
253	11	57.9	24	3	US-09-090-535-14	Sequence 14, Appl	Sequence 24, Appl	
c 254	11	57.9	24	2	US-08-495-743-47	Sequence 47, Appl	Sequence 102, App	
c 255	11	57.9	25	2	US-08-495-743-47	Sequence 47, Appl	Sequence 11, Appl	
c 256	11	57.9	25	2	US-08-495-741-47	Sequence 47, Appl	Sequence 11, Appl	
c 257	11	57.9	25	2	US-08-469-318-104	Sequence 104, App	Sequence 30, Appl	
c 258	11	57.9	25	3	US-08-468-609A-104	Sequence 104, App	Sequence 142, App	
c 259	11	57.9	25	3	US-08-062-023-47	Sequence 47, Appl	Sequence 142, App	
c 260	11	57.9	25	3	US-08-446-872A-104	Sequence 104, App	Sequence 142, App	
c 261	11	57.9	25	3	US-08-762-227A-104	Sequence 104, App	Sequence 142, App	
c 262	11	57.9	25	3	US-09-787-628-7	Sequence 7, Appli	Sequence 142, App	
c 263	11	57.9	25	3	US-08-062-021A-2	Sequence 2, Appli	Sequence 142, App	
c 264	11	57.9	25	3	US-09-510-238A-75	Sequence 75, Appl	Sequence 1, Appli	
c 265	11	57.9	25	3	US-09-721-543A-33	Sequence 33, Appl	Sequence 15, Appl	
c 266	11	57.9	25	3	US-09-721-543A-40	Sequence 40, Appl	Sequence 15, Appl	
c 267	11	57.9	25	3	US-09-675-828A-47	Sequence 47, Appl	Sequence 15, Appl	
c 268	11	57.9	25	4	US-08-957-610A-379	Sequence 379, App	Sequence 15, Appl	
c 269	11	57.9	25	7	PCT-US95-01185-104	Sequence 104, App	Sequence 15, Appl	
c 270	11	57.9	26	3	US-09-926-169-4	Sequence 4, Appli	Sequence 142, App	
c 271	11	57.9	27	2	US-07-938-334C-10	Sequence 10, Appl	Sequence 1, Appli	
272	11	57.9	27	2	US-08-145-704-14	Sequence 14, Appl	Sequence 15, Appl	
273	11	57.9	27	3	US-08-987-574-14	Sequence 14, Appl	Sequence 15, Appl	
274	11	57.9	27	3	US-08-535-168-14	Sequence 14, Appl	Sequence 15, Appl	
275	11	57.9	27	3	US-09-017-974-14	Sequence 14, Appl	Sequence 15, Appl	
276	11	57.9	27	3	US-08-682-255A-14	Sequence 14, Appl	Sequence 15, Appl	
277	11	57.9	27	3	US-09-429-130-14	Sequence 14, Appl	Sequence 3, Appli	
278	11	57.9	27	3	US-09-403-648-14	Sequence 14, Appl	Sequence 3, Appli	
279	11	57.9	27	5	US-09-543-679A-1441	Sequence 1441, Ap	Sequence 5241, Ap	
280	11	57.9	27	7	PCT-US96-11786-14	Sequence 14, Appl	Sequence 5242, Ap	
281	11	57.9	28	3	US-09-152-361A-14	Sequence 14, Appl	Sequence 5243, Ap	
282	11	57.9	28	3	US-09-304-232-367	Sequence 367, App	Sequence 5244, Ap	
283	11	57.9	29	3	US-09-304-232-553	Sequence 553, App	Sequence 5245, Ap	
284	11	57.9	29	3	US-09-647-841B-4	Sequence 4, Appli	Sequence 5246, Ap	
285	11	57.9	29	3	US-09-647-841B-5	Sequence 5, Appli	Sequence 5247, Ap	
c 286	11	57.9	29	3	US-08-592-406-27	Sequence 27, Appl	Sequence 5248, Ap	
c 287	10.8	56.8	14	4	US-09-601-326-157	Sequence 157, App	Sequence 5250, Ap	
c 288	10.8	56.8	14	4	US-10-428-826-157	Sequence 157, App	Sequence 5251, Ap	
c 289	10.8	56.8	15	2	US-08-479-248-1	Sequence 1, Appli	Sequence 5252, Ap	
c 290	10.8	56.8	15	2	US-08-479-248-2	Sequence 2, Appli	Sequence 11681, A	
c 291	10.8	56.8	15	3	US-08-557-210A-1	Sequence 1, Appli	Sequence 11693, A	
c 292	10.8	56.8	15	3	US-08-557-210A-2	Sequence 2, Appli	Sequence 7, Appli	
c 293	10.8	56.8	17	2	US-08-390-850-591	Sequence 591, App	Sequence 35600, A	
c 294	10.8	56.8	17	2	US-08-373-124A-178	Sequence 178, App	Sequence 57052, A	
c 295	10.8	56.8	17	2	US-08-435-634-591	Sequence 591, App	Sequence 86768, A	
c 296	10.8	56.8	17	2	US-08-435-628-178	Sequence 178, App	Sequence 104957, A	
c 297	10.8	56.8	17	3	US-09-474-432B-855	Sequence 855, App	Sequence 2, Appli	
c 298	10.8	56.8	17	3	US-09-476-387-854	Sequence 854, App	Sequence 11, Appl	
c 299	10.8	56.8	17	3	US-09-866-108A-2312	Sequence 2312, Ap	Sequence 12, Appl	
c 300	10.8	56.8	17	3	US-09-866-108A-2313	Sequence 2313, Ap	Sequence 13, Appl	
c 301	10.8	56.8	17	3	US-09-866-108A-2314	Sequence 2314, Ap	Sequence 16, Appl	
c 302	10.8	56.8	17	3	US-09-866-108A-2315	Sequence 2315, Ap	Sequence 21, Appl	
c 303	10.8	56.8	17	3	US-09-866-108A-6789	Sequence 6789, Ap	Sequence 21, Appl	
c 304	10.8	56.8	17	3	US-09-866-108A-6793	Sequence 6793, Ap	Sequence 2, Appli	
c 305	10.8	56.8	17	4	US-10-222-825-6	Sequence 6, Appli	Sequence 2, Appli	
c 306	10.8	56.8	18	3	US-09-544-398B-475	Sequence 475, App	Sequence 16, Appl	
c 307	10.8	56.8	18	3	US-09-543-771B-475	Sequence 475, App	Sequence 17, Appl	
c 308	10.8	56.8	18	4	US-09-331-204A-5	Sequence 5, Appli	Sequence 17, Appl	
c 309	10.8	56.8	18	4	US-09-331-204A-20	Sequence 20, Appl	Sequence 5, Appli	
c 310	10.8	56.8	19	3	US-08-422-978-6862	Sequence 6862, Ap	Sequence 5, Appli	
c 311	10.8	56.8	20	2	US-08-263-413-11	Sequence 11, Appl	Sequence 6, Appli	
c 312	10.8	56.8	20	3	US-09-433-694-20	Sequence 20, Appl	Sequence 3, Appli	
c 313	10.8	56.8	20	3	US-09-490-692-123	Sequence 123, App	Sequence 34, Appl	
c 314	10.8	56.8	20	3	US-09-658-688A-47	Sequence 47, Appl	Sequence 22, Appl	
c 315	10.8	56.8	20	3	US-09-198-452A-4824	Sequence 4824, Ap	Sequence 7077, Ap	

389	10.6	55.8	17	7	PCT-US94-02471-34	Sequence 34, Appl	462	10.6	55.8	24	3	US-09-918-686-96	Sequence 96, Appl
390	10.6	55.8	18	3	US-09-216-393B-147	Sequence 147, App	463	10.6	55.8	24	3	US-08-559-390-437	Sequence 437, App
C 391	10.6	55.8	19	3	US-09-375-318-27	Sequence 27, Appl	464	10.6	55.8	24	3	US-08-899-112B-3	Sequence 3, Appl
C 392	10.6	55.8	19	3	US-09-696-791-3414	Sequence 3414, Ap	C 465	10.6	55.8	24	3	US-09-786-569-5	Sequence 5, Appl
393	10.6	55.8	20	2	US-08-031-147A-6	Sequence 6, Appl	466	10.6	55.8	24	3	US-10-106-275-13	Sequence 13, Appl
394	10.6	55.8	20	2	US-08-031-147A-11	Sequence 11, Appl	467	10.6	55.8	24	3	US-09-011-553-10	Sequence 10, Appl
395	10.6	55.8	20	2	US-08-031-147A-12	Sequence 12, Appl	468	10.6	55.8	24	5	US-10-007-132-20	Sequence 20, Appl
C 396	10.6	55.8	20	2	US-08-089-996-1	Sequence 1, Appl	469	10.6	55.8	24	5	US-10-007-132-33	Sequence 33, Appl
C 397	10.6	55.8	20	2	US-08-171-718-3	Sequence 3, Appl	470	10.6	55.8	24	7	PCT-US93-11198-437	Sequence 437, App
C 398	10.6	55.8	20	2	US-08-525-697-9	Sequence 9, Appl	471	10.6	55.8	25	3	US-08-822-440-30	Sequence 30, Appl
C 399	10.6	55.8	20	2	US-08-557-139-28	Sequence 28, Appl	472	10.6	55.8	25	3	US-09-396-540-30	Sequence 30, Appl
C 400	10.6	55.8	20	2	US-08-478-178A-1	Sequence 1, Appl	C 473	10.6	55.8	25	3	US-09-402-631A-27	Sequence 27, Appl
C 401	10.6	55.8	20	2	US-08-488-177-1	Sequence 1, Appl	474	10.6	55.8	25	3	US-09-396-196G-23085	Sequence 23085, A
C 402	10.6	55.8	20	2	US-08-481-072A-1	Sequence 1, Appl	C 475	10.6	55.8	25	3	US-09-396-196G-23385	Sequence 23385, A
C 403	10.6	55.8	20	2	US-08-664-336-1	Sequence 1, Appl	C 476	10.6	55.8	25	3	US-09-396-196G-28220	Sequence 28220, A
C 404	10.6	55.8	20	2	US-08-403-888A-21	Sequence 21, Appl	C 477	10.6	55.8	25	3	US-09-396-196G-36400	Sequence 36400, A
405	10.6	55.8	20	2	US-08-403-888A-127	Sequence 127, App	C 478	10.6	55.8	25	3	US-09-396-196G-37039	Sequence 37039, A
406	10.6	55.8	20	2	US-08-403-888A-128	Sequence 128, App	C 479	10.6	55.8	25	3	US-09-396-196G-37040	Sequence 37040, A
C 407	10.6	55.8	20	2	US-08-481-066A-1	Sequence 1, Appl	C 480	10.6	55.8	25	3	US-09-396-196G-51781	Sequence 51781, A
C 408	10.6	55.8	20	2	US-08-476-712-2	Sequence 2, Appl	481	10.6	55.8	25	3	US-09-396-196G-58972	Sequence 58972, A
C 409	10.6	55.8	20	3	US-08-578-615A-1	Sequence 1, Appl	C 482	10.6	55.8	25	3	US-09-396-196G-96021	Sequence 96021, A
C 410	10.6	55.8	20	3	US-08-578-615A-120	Sequence 120, App	C 483	10.6	55.8	25	3	US-09-396-196G-113561	Sequence 113561, A
C 411	10.6	55.8	20	3	US-08-478-087-3	Sequence 3, Appl	C 484	10.6	55.8	25	3	US-09-396-196G-113562	Sequence 113562, A
C 412	10.6	55.8	20	3	US-09-428-696-31	Sequence 31, Appl	C 485	10.6	55.8	25	3	US-09-396-196G-113563	Sequence 113563, A
C 413	10.6	55.8	20	3	US-09-031-006-12	Sequence 12, Appl	486	10.6	55.8	26	3	US-09-268-163-26	Sequence 26, Appl
C 414	10.6	55.8	20	3	US-09-225-749-1	Sequence 1, Appl	C 487	10.6	55.8	26	3	US-10-012-231A-452	Sequence 452, App
C 415	10.6	55.8	20	3	US-09-411-231-2	Sequence 2, Appl	C 488	10.6	55.8	26	3	US-09-622-745B-22	Sequence 22, Appl
C 416	10.6	55.8	20	3	US-08-829-637A-1	Sequence 1, Appl	C 489	10.6	55.8	26	3	US-09-622-745B-23	Sequence 23, Appl
C 417	10.6	55.8	20	3	US-09-851-520-19	Sequence 19, Appl	C 490	10.6	55.8	26	3	US-10-015-389A-452	Sequence 452, App
C 418	10.6	55.8	20	3	US-08-802-331-31	Sequence 31, Appl	C 491	10.6	55.8	26	3	US-10-006-768A-452	Sequence 452, App
C 419	10.6	55.8	20	3	US-09-806-254-14	Sequence 14, Appl	C 492	10.6	55.8	26	3	US-10-015-671A-452	Sequence 452, App
C 420	10.6	55.8	20	3	US-09-254-322-1	Sequence 1, Appl	C 493	10.6	55.8	26	3	US-10-015-393A-452	Sequence 452, App
C 421	10.6	55.8	20	3	US-10-025-139-1	Sequence 1, Appl	C 494	10.6	55.8	26	3	US-10-011-833A-452	Sequence 452, App
C 422	10.6	55.8	20	3	US-09-780-045-31	Sequence 31, Appl	C 495	10.6	55.8	26	3	US-10-006-041A-452	Sequence 452, App
423	10.6	55.8	20	3	US-09-922-271-12	Sequence 12, Appl	C 496	10.6	55.8	26	3	US-10-012-064A-452	Sequence 452, App
424	10.6	55.8	20	3	US-09-845-917-1	Sequence 1, Appl	C 497	10.6	55.8	26	4	US-10-015-392A-452	Sequence 452, App
C 425	10.6	55.8	20	3	US-09-864-894C-10	Sequence 10, Appl	C 498	10.6	55.8	26	5	US-10-011-795B-452	Sequence 452, App
C 426	10.6	55.8	20	3	US-09-864-894C-11	Sequence 11, Appl	499	10.6	55.8	26	5	US-10-033-026-26	Sequence 26, Appl
C 427	10.6	55.8	20	3	US-09-863-049B-49	Sequence 49, Appl	C 500	10.6	55.8	26	5	US-10-015-386A-452	Sequence 452, App
C 428	10.6	55.8	20	3	US-09-269-446D-49	Sequence 49, Appl	C 501	10.6	55.8	26	5	US-10-012-121A-452	Sequence 452, App
C 429	10.6	55.8	20	7	PCT-US93-02213-1	Sequence 1, Appl	C 502	10.6	55.8	26	5	US-10-006-485A-452	Sequence 452, App
430	10.6	55.8	20	7	PCT-US94-02471-6	Sequence 6, Appl	C 503	10.6	55.8	26	5	US-10-006-746A-452	Sequence 452, App
431	10.6	55.8	20	7	PCT-US94-02471-11	Sequence 11, Appl	C 504	10.6	55.8	26	5	US-10-012-752A-452	Sequence 452, App
432	10.6	55.8	20	7	PCT-US94-02471-12	Sequence 12, Appl	C 505	10.6	55.8	26	5	US-10-017-253A-452	Sequence 452, App
C 433	10.6	55.8	20	7	PCT-US94-07770-1	Sequence 1, Appl	C 506	10.6	55.8	26	5	US-10-015-515A-452	Sequence 452, App
434	10.6	55.8	21	3	US-08-594-452-78	Sequence 78, Appl	C 507	10.6	55.8	26	5	US-10-015-715A-452	Sequence 452, App
435	10.6	55.8	21	3	US-09-258-408-78	Sequence 78, Appl	C 508	10.6	55.8	26	5	US-10-007-236A-452	Sequence 452, App
436	10.6	55.8	21	3	US-09-230-704-9	Sequence 9, Appl	C 509	10.6	55.8	27	3	US-07-807-529A-54	Sequence 54, Appl
437	10.6	55.8	21	3	US-09-609-162-9	Sequence 9, Appl	C 510	10.6	55.8	27	3	US-08-513-974B-163	Sequence 163, App
438	10.6	55.8	21	3	US-09-634-732-9	Sequence 9, Appl	511	10.6	55.8	27	3	US-09-164-210-14	Sequence 14, Appl
439	10.6	55.8	21	3	US-09-859-053-9	Sequence 9, Appl	512	10.6	55.8	28	3	US-09-197-218-5	Sequence 5, Appl
C 440	10.6	55.8	21	3	US-10-048-882C-11	Sequence 11, Appl	513	10.6	55.8	29	3	US-08-840-062-13	Sequence 13, Appl
C 441	10.6	55.8	21	5	US-10-349-852-5	Sequence 5, Appl	C 514	10.6	55.8	29	3	US-08-467-126-1	Sequence 1, Appl
C 442	10.6	55.8	22	3	US-08-974-549A-496	Sequence 496, App	515	10.6	55.8	30	2	US-08-476-712-3	Sequence 3, Appl
C 443	10.6	55.8	22	3	US-09-203-895-8	Sequence 8, Appl	516	10.6	55.8	30	2	US-08-341-560B-30	Sequence 30, Appl
C 444	10.6	55.8	22	3	US-08-912-951-263	Sequence 263, App	C 517	10.6	55.8	30	3	US-08-983-075D-2	Sequence 2, Appl
C 445	10.6	55.8	22	3	US-09-402-181B-496	Sequence 496, App	518	10.6	55.8	30	3	US-09-411-291-3	Sequence 3, Appl
C 446	10.6	55.8	22	3	US-09-721-456-496	Sequence 496, App	519	10.6	55.8	30	3	US-08-983-075D-2	Sequence 2, Appl
C 447	10.6	55.8	22	3	US-09-283-909-14	Sequence 14, Appl	520	10.6	55.8	30	3	US-09-052-919-50	Sequence 50, Appl
C 448	10.6	55.8	22	4	US-09-762-278-9	Sequence 9, Appl	521	10.6	55.8	30	3	US-09-953-052-50	Sequence 50, Appl
C 449	10.6	55.8	23	2	US-08-347-343-1	Sequence 1, Appl	522	10.6	55.8	30	10	5245022-25	Patent No. 5245022
450	10.6	55.8	23	3	US-07-808-452-15	Sequence 15, Appl	C 523	10.4	54.7	13	2	US-08-250-740-31	Sequence 31, Appl
451	10.6	55.8	23	7	PCT-US92-10770-15	Sequence 15, Appl	C 524	10.4	54.7	14	3	US-09-328-174A-20	Sequence 20, Appl
452	10.6	55.8	23	7	PCT-US92-10792-13	Sequence 13, Appl	C 525	10.4	54.7	17	2	US-08-250-740-13	Sequence 13, Appl
453	10.6	55.8	24	2	US-08-411-796-437	Sequence 437, App	C 526	10.4	54.7	17	3	US-09-686-597-21	Sequence 21, Appl
454	10.6	55.8	24	2	US-08-626-685A-3	Sequence 3, Appl	527	10.4	54.7	17	3	US-09-866-108A-6787	Sequence 6787, Ap
455	10.6	55.8	24	3	US-08-594-452-79	Sequence 79, Appl	528	10.4	54.7	17	3	US-09-866-108A-6788	Sequence 6788, Ap
456	10.6	55.8	24	3	US-08-471-039-437	Sequence 437, App	C 529	10.4	54.7	18	3	US-09-493-565-7	Sequence 7, Appl
457	10.6	55.8	24	3	US-09-258-408-79	Sequence 79, Appl	530	10.4	54.7	18	3	US-09-422-7812-7812	Sequence 7812, Ap
458	10.6	55.8	24	3	US-09-199-737-20	Sequence 20, Appl	C 531	10.4	54.7	19	2	US-08-222-177A-299	Sequence 299, App
459	10.6	55.8	24	3	US-09-199-737-33	Sequence 33, Appl	532	10.4	54.7	19	2	US-08-631-200-47	Sequence 47, Appl
460	10.6	55.8	24	3	US-09-058-333A-20	Sequence 20, Appl	533	10.4	54.7	19	2	US-08-823-553-47	Sequence 47, Appl
461	10.6	55.8	24	3	US-09-058-333A-33	Sequence 33, Appl	534	10.4	54.7	19	2	US-08-922-267A-47	Sequence 47, Appl

535	10.4	54.7	19	2	US-08-936-707A-47	Sequence 47, Appl	c 608	10.2	53.7	17	3	US-09-371-772B-2368	Sequence 2368, Ap
536	10.4	54.7	19	2	US-08-936-706A-47	Sequence 47, Appl	609	10.2	53.7	17	3	US-09-476-387-820	Sequence 820, App
537	10.4	54.7	19	3	US-09-248-203-47	Sequence 47, Appl	c 610	10.2	53.7	17	3	US-09-476-387-838	Sequence 838, App
538	10.4	54.7	19	3	US-09-406-071-47	Sequence 47, Appl	611	10.2	53.7	17	3	US-09-866-108A-895	Sequence 895, App
539	10.4	54.7	19	3	US-09-814-986-47	Sequence 47, Appl	612	10.2	53.7	17	3	US-09-866-108A-896	Sequence 896, App
c 540	10.4	54.7	19	3	US-10-164-230-59	Sequence 59, Appl	613	10.2	53.7	17	3	US-09-866-108A-897	Sequence 897, App
c 541	10.4	54.7	20	2	US-08-487-141B-63	Sequence 63, Appl	614	10.2	53.7	17	3	US-10-059-877-26	Sequence 26, Appl
c 542	10.4	54.7	20	2	US-08-512-681-22	Sequence 22, Appl	c 615	10.2	53.7	17	3	US-09-685-664B-2368	Sequence 2368, Ap
c 543	10.4	54.7	20	2	US-08-927-561-63	Sequence 63, Appl	616	10.2	53.7	17	5	US-10-156-306B-2329	Sequence 2329, Ap
544	10.4	54.7	20	3	US-08-991-426-15	Sequence 15, Appl	617	10.2	53.7	17	5	US-10-156-306B-3652	Sequence 3652, Ap
545	10.4	54.7	20	3	US-09-143-470-11	Sequence 11, Appl	c 618	10.2	53.7	17	5	US-10-138-674B-2368	Sequence 2368, Ap
546	10.4	54.7	20	3	US-08-753-007A-30	Sequence 30, Appl	619	10.2	53.7	18	2	US-08-424-663-6	Sequence 6, Appli
547	10.4	54.7	20	3	US-09-398-496-30	Sequence 30, Appl	c 620	10.2	53.7	18	2	US-08-311-486C-1060	Sequence 1060, Ap
548	10.4	54.7	20	3	US-09-052-995-13	Sequence 13, Appl	c 621	10.2	53.7	18	2	US-08-311-486C-1143	Sequence 1143, Ap
549	10.4	54.7	20	3	US-09-536-259-9	Sequence 9, Appli	622	10.2	53.7	18	2	US-08-529-878B-3	Sequence 3, Appli
550	10.4	54.7	20	3	US-09-980-052-81	Sequence 81, Appl	623	10.2	53.7	18	2	US-08-529-878B-44	Sequence 44, Appl
551	10.4	54.7	20	3	US-09-856-371A-27	Sequence 27, Appl	624	10.2	53.7	18	2	US-08-726-012B-8	Sequence 8, Appli
c 552	10.4	54.7	20	3	US-10-002-623-23	Sequence 23, Appl	625	10.2	53.7	18	2	US-09-161-015-45	Sequence 45, Appl
c 553	10.4	54.7	20	7	PCR-US96-09388-63	Sequence 63, Appl	626	10.2	53.7	18	2	US-08-872-446-6	Sequence 6, Appli
c 554	10.4	54.7	21	3	US-09-382-552-185	Sequence 185, App	c 627	10.2	53.7	18	2	US-08-872-446-10	Sequence 10, Appl
555	10.4	54.7	21	3	US-09-657-472-1426	Sequence 1426, Ap	628	10.2	53.7	18	3	US-09-280-409-58	Sequence 58, Appl
556	10.4	54.7	22	3	US-09-745-129-2	Sequence 2, Appli	c 629	10.2	53.7	18	3	US-09-025-701-4	Sequence 4, Appli
c 557	10.4	54.7	23	3	US-08-849-602C-14	Sequence 14, Appl	c 630	10.2	53.7	18	3	US-09-630-706-55	Sequence 55, Appl
c 558	10.4	54.7	23	3	US-09-046-894-14	Sequence 14, Appl	631	10.2	53.7	18	3	US-09-280-270A-6	Sequence 6, Appli
559	10.4	54.7	24	3	US-09-255-518C-37	Sequence 37, Appl	c 632	10.2	53.7	18	3	US-09-280-270A-10	Sequence 10, Appl
c 560	10.4	54.7	24	3	US-10-112-802-14	Sequence 14, Appl	c 633	10.2	53.7	18	3	US-09-167-109-34	Sequence 34, Appl
c 561	10.4	54.7	24	3	US-10-112-802-18	Sequence 18, Appl	634	10.2	53.7	18	3	US-09-387-341-188	Sequence 188, App
c 562	10.4	54.7	24	3	US-09-981-953A-13	Sequence 13, Appl	635	10.2	53.7	18	3	US-09-725-265-46	Sequence 46, Appl
563	10.4	54.7	25	3	US-09-866-108A-11679	Sequence 11679, A	c 636	10.2	53.7	18	3	US-09-725-265-50	Sequence 50, Appl
564	10.4	54.7	25	3	US-09-866-108A-11680	Sequence 11680, A	c 637	10.2	53.7	18	3	US-09-422-978-7437	Sequence 7437, Ap
c 565	10.4	54.7	25	3	US-09-396-196G-75137	Sequence 75137, A	c 638	10.2	53.7	18	3	US-09-556-137-46	Sequence 46, Appl
566	10.4	54.7	25	3	US-09-396-196G-118171	Sequence 118171, A	639	10.2	53.7	18	3	US-09-556-137-46	Sequence 46, Appl
567	10.4	54.7	26	2	US-08-971-773-69	Sequence 69, Appl	c 640	10.2	53.7	18	4	US-09-556-127-50	Sequence 50, Appl
568	10.4	54.7	26	2	US-08-254-114A-3	Sequence 3, Appli	641	10.2	53.7	18	4	US-09-331-204A-4	Sequence 4, Appli
569	10.4	54.7	26	2	US-08-721-260-12	Sequence 12, Appl	642	10.2	53.7	18	4	US-09-331-204A-8	Sequence 8, Appli
570	10.4	54.7	26	3	US-08-818-082-1	Sequence 1, Appli	643	10.2	53.7	19	3	US-08-860-038-6	Sequence 6, Appli
571	10.4	54.7	26	3	US-08-997-685A-26	Sequence 26, Appl	644	10.2	53.7	19	3	US-08-580-923-6	Sequence 6, Appli
572	10.4	54.7	26	3	US-09-692-056-1	Sequence 1, Appli	c 645	10.2	53.7	19	3	US-09-387-341-198	Sequence 198, App
573	10.4	54.7	27	2	US-08-410-654B-44	Sequence 44, Appl	646	10.2	53.7	19	3	US-09-153-838-10	Sequence 10, Appl
574	10.4	54.7	27	2	US-08-478-851-44	Sequence 44, Appl	c 647	10.2	53.7	19	3	US-09-975-123-4	Sequence 4, Appli
575	10.4	54.7	27	2	US-08-481-560-44	Sequence 44, Appl	648	10.2	53.7	19	3	US-09-696-731-528	Sequence 528, App
576	10.4	54.7	27	2	US-08-607-509-13	Sequence 13, Appl	649	10.2	53.7	19	10	5352575-10	Patent No. 5352575
577	10.4	54.7	27	2	US-08-634-642-13	Sequence 13, Appl	650	10.2	53.7	20	2	US-07-922-723A-53	Sequence 53, Appl
578	10.4	54.7	27	2	US-08-483-511-72	Sequence 72, Appl	651	10.2	53.7	20	2	US-07-799-828C-53	Sequence 53, Appl
579	10.4	54.7	27	3	US-09-403-066A-8	Sequence 8, Appli	652	10.2	53.7	20	2	US-08-031-147A-9	Sequence 9, Appli
580	10.4	54.7	27	3	US-09-086-436-14	Sequence 14, Appl	653	10.2	53.7	20	2	US-08-031-147A-10	Sequence 10, Appl
581	10.4	54.7	27	3	US-09-086-436-26	Sequence 26, Appl	654	10.2	53.7	20	2	US-08-031-147A-47	Sequence 47, Appl
c 582	10.4	54.7	27	3	US-09-723-000A-11	Sequence 11, Appli	655	10.2	53.7	20	2	US-08-031-147A-51	Sequence 51, Appl
583	10.4	54.7	28	3	US-09-121-539-2	Sequence 2, Appli	656	10.2	53.7	20	2	US-08-031-143B-63	Sequence 63, Appl
584	10.4	54.7	28	3	US-09-117-860-40	Sequence 40, Appl	657	10.2	53.7	20	2	US-08-555-678-49	Sequence 49, Appl
585	10.4	54.7	28	3	US-09-117-860-40	Sequence 40, Appl	658	10.2	53.7	20	2	US-08-173-489C-17	Sequence 17, Appl
586	10.4	54.7	29	3	US-09-304-232-381	Sequence 381, App	659	10.2	53.7	20	2	US-07-952-277A-53	Sequence 53, Appl
587	10.4	54.7	29	3	US-09-830-967-2	Sequence 2, Appli	c 660	10.2	53.7	20	2	US-08-529-878B-23	Sequence 23, Appl
588	10.4	54.7	29	10	521286-68	Patent No. 521286	661	10.2	53.7	20	2	US-08-403-888A-125	Sequence 125, App
c 589	10.2	53.7	15	2	US-08-291-932A-378	Sequence 378, App	662	10.2	53.7	20	2	US-08-403-888A-126	Sequence 126, App
590	10.2	53.7	15	2	US-08-856-141-20	Sequence 20, Appl	663	10.2	53.7	20	2	US-08-403-888A-137	Sequence 137, App
591	10.2	53.7	15	3	US-09-495-140-20	Sequence 20, Appl	664	10.2	53.7	20	2	US-08-403-888A-141	Sequence 141, App
592	10.2	53.7	15	3	US-10-059-877-20	Sequence 20, Appl	c 665	10.2	53.7	20	2	US-09-048-804-6	Sequence 6, Appli
593	10.2	53.7	15	4	US-09-341-700A-140	Sequence 140, App	c 666	10.2	53.7	20	3	US-09-429-323-46	Sequence 46, Appl
c 594	10.2	53.7	16	2	US-08-357-589-3	Sequence 3, Appli	c 667	10.2	53.7	20	3	US-08-765-340-30	Sequence 30, Appl
c 595	10.2	53.7	16	2	US-09-003-289-3	Sequence 3, Appli	668	10.2	53.7	20	3	US-09-313-932-275	Sequence 275, App
596	10.2	53.7	16	3	US-08-856-141-22	Sequence 22, Appli	c 669	10.2	53.7	20	3	US-09-662-249A-44	Sequence 44, Appl
597	10.2	53.7	16	3	US-09-479-524-6	Sequence 6, Appli	670	10.2	53.7	20	3	US-09-393-529-16	Sequence 16, Appl
598	10.2	53.7	16	3	US-09-495-140-22	Sequence 22, Appl	671	10.2	53.7	20	3	US-09-422-978-5435	Sequence 5435, Ap
599	10.2	53.7	16	3	US-10-059-877-22	Sequence 22, Appl	672	10.2	53.7	20	3	US-09-422-978-5858	Sequence 5858, Ap
c 600	10.2	53.7	16	7	PCR-US95-16435-3	Sequence 3, Appli	673	10.2	53.7	20	3	US-09-422-978-5972	Sequence 5972, Ap
c 601	10.2	53.7	17	2	US-08-173-489C-8	Sequence 8, Appli	674	10.2	53.7	20	3	US-09-422-978-7145	Sequence 7145, Ap
c 602	10.2	53.7	17	2	US-08-173-489C-92	Sequence 92, Appl	c 675	10.2	53.7	20	3	US-09-432-978-10500	Sequence 10500, A
c 603	10.2	53.7	17	3	US-08-998-099-47	Sequence 47, Appl	676	10.2	53.7	20	3	US-09-198-452A-4432	Sequence 4432, Ap
c 604	10.2	53.7	17	3	US-08-584-040-5477	Sequence 5477, Ap	c 677	10.2	53.7	20	3	US-09-198-452A-6147	Sequence 6147, Ap
605	10.2	53.7	17	3	US-09-495-140-26	Sequence 26, Appl	c 678	10.2	53.7	20	3	US-09-198-452A-6561	Sequence 6561, Ap
c 606	10.2	53.7	17	3	US-09-474-432B-821	Sequence 821, App	c 679	10.2	53.7	20	3	US-09-486-147-28	Sequence 28, Appl
c 607	10.2	53.7	17	3	US-09-474-432B-839	Sequence 839, App	680	10.2	53.7	20	3	US-09-486-147-29	Sequence 29, Appl

681	10.2	53.7	20	3	US-09-232-785-215	Sequence 215, App	754	10.2	53.7	24	3	US-10-012-231A-13	Sequence 13, Appl
c 682	10.2	53.7	20	3	US-09-866-5708-38	Sequence 38, Appl	755	10.2	53.7	24	3	US-10-015-368A-13	Sequence 13, Appl
683	10.2	53.7	20	3	US-09-863-049B-18	Sequence 18, Appl	756	10.2	53.7	24	3	US-10-006-768A-13	Sequence 13, Appl
c 684	10.2	53.7	20	3	US-09-263-446B-53	Sequence 53, Appl	757	10.2	53.7	24	3	US-10-015-671A-13	Sequence 13, Appl
685	10.2	53.7	20	3	PCT-US94-02471-9	Sequence 9, Appl	758	10.2	53.7	24	3	US-10-015-393A-13	Sequence 13, Appl
686	10.2	53.7	20	7	PCT-US94-02471-10	Sequence 10, Appl	759	10.2	53.7	24	3	US-10-011-833A-13	Sequence 13, Appl
687	10.2	53.7	20	7	PCT-US94-02471-10	Sequence 47, Appl	760	10.2	53.7	24	3	US-10-006-041A-13	Sequence 13, Appl
688	10.2	53.7	20	7	PCT-US94-02471-11	Sequence 51, Appl	761	10.2	53.7	24	3	US-10-012-064A-13	Sequence 13, Appl
689	10.2	53.7	20	7	PCT-US94-02891-63	Sequence 63, Appl	762	10.2	53.7	24	4	US-10-015-392A-13	Sequence 13, Appl
690	10.2	53.7	20	10	5352575-12	Patent No. 5352575	763	10.2	53.7	24	5	US-10-011-795B-13	Sequence 13, Appl
691	10.2	53.7	21	2	US-08-271-946A-8	Sequence 8, Appl	764	10.2	53.7	24	5	US-10-015-386A-13	Sequence 13, Appl
692	10.2	53.7	21	2	US-08-271-942A-8	Sequence 8, Appl	765	10.2	53.7	24	5	US-10-012-121A-13	Sequence 13, Appl
693	10.2	53.7	21	2	US-08-319-836B-25	Sequence 25, Appl	766	10.2	53.7	24	5	US-10-006-485A-13	Sequence 13, Appl
694	10.2	53.7	21	2	US-08-635-309-25	Sequence 25, Appl	767	10.2	53.7	24	5	US-10-006-746A-13	Sequence 13, Appl
695	10.2	53.7	21	2	US-08-505-509-11	Sequence 11, Appl	768	10.2	53.7	24	5	US-10-012-752A-13	Sequence 13, Appl
696	10.2	53.7	21	2	US-08-580-038-56	Sequence 56, Appl	769	10.2	53.7	24	5	US-10-017-253A-13	Sequence 13, Appl
697	10.2	53.7	21	2	US-08-491-690A-11	Sequence 11, Appl	770	10.2	53.7	24	5	US-10-015-715A-13	Sequence 13, Appl
698	10.2	53.7	21	2	US-08-845-998-12	Sequence 12, Appl	771	10.2	53.7	24	5	US-10-015-715A-13	Sequence 13, Appl
699	10.2	53.7	21	2	US-08-529-878B-4	Sequence 4, Appl	772	10.2	53.7	24	5	US-10-007-236A-13	Sequence 13, Appl
700	10.2	53.7	21	2	US-08-529-878B-45	Sequence 45, Appl	773	10.2	53.7	24	7	PCT-US95-13608-22	Sequence 22, Appl
701	10.2	53.7	21	3	US-08-773-916A-8	Sequence 8, Appl	774	10.2	53.7	24	10	5245022-9	Patent No. 5245022
c 702	10.2	53.7	21	3	US-09-009-913-74	Sequence 74, Appl	775	10.2	53.7	25	2	US-08-324-465-7	Sequence 7, Appl
703	10.2	53.7	21	3	US-09-206-537-12	Sequence 12, Appl	776	10.2	53.7	25	2	US-08-401-512-28	Sequence 28, Appl
704	10.2	53.7	21	3	US-08-750-232-8	Sequence 8, Appl	777	10.2	53.7	25	2	US-08-641-627A-17	Sequence 17, Appl
705	10.2	53.7	21	3	US-09-430-854-12	Sequence 12, Appl	778	10.2	53.7	25	2	US-08-641-627A-18	Sequence 18, Appl
c 706	10.2	53.7	21	3	US-08-949-344C-20	Sequence 20, Appl	779	10.2	53.7	25	2	US-08-641-627A-19	Sequence 19, Appl
c 707	10.2	53.7	21	3	US-09-553-690-17	Sequence 17, Appl	780	10.2	53.7	25	2	US-08-465-981-7	Sequence 7, Appl
708	10.2	53.7	21	3	US-09-113-507B-55	Sequence 55, Appl	c 781	10.2	53.7	25	3	US-08-737-607-31	Sequence 31, Appl
c 709	10.2	53.7	21	3	US-09-380-836-90	Sequence 90, Appl	782	10.2	53.7	25	3	US-09-226-012-16	Sequence 16, Appl
710	10.2	53.7	21	3	US-08-897-556A-55	Sequence 55, Appl	783	10.2	53.7	25	3	US-08-776-971-78	Sequence 78, Appl
711	10.2	53.7	21	3	US-09-547-693-55	Sequence 55, Appl	784	10.2	53.7	25	3	US-09-866-108A-3824	Sequence 3824, Ap
c 712	10.2	53.7	21	3	US-09-657-472-1093	Sequence 1093, Ap	785	10.2	53.7	25	3	US-09-866-108A-3825	Sequence 3825, Ap
c 713	10.2	53.7	21	3	US-09-657-472-1096	Sequence 1956, Ap	786	10.2	53.7	25	3	US-09-866-108A-3826	Sequence 3826, Ap
c 714	10.2	53.7	21	3	US-09-684-061-10	Sequence 10, Appl	787	10.2	53.7	25	3	US-09-866-108A-3827	Sequence 3827, Ap
715	10.2	53.7	21	4	US-09-331-204A-6	Sequence 6, Appl	788	10.2	53.7	25	3	US-09-866-108A-3828	Sequence 3828, Ap
716	10.2	53.7	21	7	PCT-US95-08604-8	Sequence 8, Appl	789	10.2	53.7	25	3	US-09-866-108A-3829	Sequence 3829, Ap
717	10.2	53.7	21	7	PCT-US95-08606-8	Sequence 8, Appl	790	10.2	53.7	25	3	US-09-866-108A-3830	Sequence 3830, Ap
718	10.2	53.7	21	7	PCT-US95-13142-25	Sequence 25, Appl	791	10.2	53.7	25	3	US-09-866-108A-3831	Sequence 3831, Ap
719	10.2	53.7	22	3	US-08-435-350-81	Sequence 81, Appl	792	10.2	53.7	25	3	US-09-866-108A-3832	Sequence 3832, Ap
c 720	10.2	53.7	22	3	US-09-043-149-7	Sequence 7, Appl	793	10.2	53.7	25	3	US-09-866-108A-3833	Sequence 3833, Ap
c 721	10.2	53.7	23	3	US-09-061-768A-24	Sequence 24, Appl	794	10.2	53.7	25	3	US-09-866-108A-3834	Sequence 3834, Ap
c 722	10.2	53.7	23	3	US-09-537-357-37	Sequence 37, Appl	c 795	10.2	53.7	25	3	US-09-576-290-78	Sequence 78, Appl
c 723	10.2	53.7	23	3	US-09-764-246-24	Sequence 24, Appl	c 796	10.2	53.7	25	3	US-09-396-196G-9051	Sequence 9051, Ap
724	10.2	53.7	23	3	US-09-999-833A-165	Sequence 165, App	c 797	10.2	53.7	25	3	US-09-396-196G-24441	Sequence 24441, A
725	10.2	53.7	23	3	US-10-020-445A-165	Sequence 165, App	c 798	10.2	53.7	25	3	US-09-396-196G-24442	Sequence 24442, A
726	10.2	53.7	23	4	US-09-978-189-165	Sequence 165, App	c 799	10.2	53.7	25	3	US-09-396-196G-50205	Sequence 50205, A
727	10.2	53.7	23	5	US-10-017-085A-165	Sequence 165, App	c 800	10.2	53.7	25	3	US-09-396-196G-50205	Sequence 50205, A
728	10.2	53.7	23	5	US-10-145-129A-165	Sequence 165, App	c 801	10.2	53.7	25	3	US-09-396-196G-67755	Sequence 67755, A
729	10.2	53.7	23	5	US-10-013-929A-165	Sequence 165, App	c 802	10.2	53.7	25	3	US-09-396-196G-73046	Sequence 73046, A
730	10.2	53.7	23	5	US-10-013-917A-165	Sequence 165, App	c 803	10.2	53.7	25	3	US-09-396-196G-77918	Sequence 77918, A
731	10.2	53.7	24	2	US-08-466-033-222	Sequence 222, App	c 804	10.2	53.7	25	3	US-09-396-196G-80769	Sequence 80769, A
732	10.2	53.7	24	2	US-08-444-733-222	Sequence 222, App	c 805	10.2	53.7	25	3	US-09-396-196G-80943	Sequence 80943, A
733	10.2	53.7	24	2	US-08-464-134-222	Sequence 22, App	c 806	10.2	53.7	25	3	US-09-396-196G-87940	Sequence 87940, A
734	10.2	53.7	24	2	US-08-477-890-1	Sequence 1, Appl	c 807	10.2	53.7	25	3	US-09-396-196G-87941	Sequence 87941, A
735	10.2	53.7	24	2	US-08-461-361-222	Sequence 222, App	c 808	10.2	53.7	25	3	US-09-396-196G-103041	Sequence 103041, A
736	10.2	53.7	24	2	US-08-485-910-222	Sequence 222, App	c 809	10.2	53.7	25	3	US-09-396-196G-114702	Sequence 114702, A
737	10.2	53.7	24	2	US-08-467-034A-1	Sequence 1, Appl	c 810	10.2	53.7	25	3	US-09-396-196G-119048	Sequence 119048, A
738	10.2	53.7	24	3	US-09-176-862-15	Sequence 15, Appl	c 811	10.2	53.7	25	3	US-09-396-196G-119049	Sequence 119049, A
739	10.2	53.7	24	3	US-09-132-849-2	Sequence 2, Appl	c 812	10.2	53.7	25	3	US-09-396-196G-121128	Sequence 121128, A
740	10.2	53.7	24	3	US-09-327-229-22	Sequence 22, Appl	c 813	10.2	53.7	25	3	US-10-232-459-6	Sequence 6, Appl
741	10.2	53.7	24	3	US-08-468-646A-1	Sequence 1, Appl	c 814	10.2	53.7	25	7	PCT-US93-11915-7	Sequence 7, Appl
742	10.2	53.7	24	3	US-08-818-082-4	Sequence 4, Appl	815	10.2	53.7	26	2	US-08-770-565-25	Sequence 25, Appl
743	10.2	53.7	24	3	US-09-115-387-2	Sequence 2, Appl	816	10.2	53.7	26	2	US-08-887-798-22	Sequence 22, Appl
744	10.2	53.7	24	3	US-09-369-912-6	Sequence 6, Appl	817	10.2	53.7	26	2	US-08-785-340-4	Sequence 4, Appl
c 745	10.2	53.7	24	3	US-08-455-014B-1	Sequence 1, Appl	818	10.2	53.7	26	3	US-09-720-435A-486	Sequence 486, App
746	10.2	53.7	24	3	US-08-471-645A-1	Sequence 1, Appl	c 819	10.2	53.7	26	3	US-09-998-976-6	Sequence 6, Appl
747	10.2	53.7	24	3	US-09-692-056-4	Sequence 4, Appl	820	10.2	53.7	26	2	US-08-647-584-20	Sequence 20, Appl
748	10.2	53.7	24	3	US-10-144-669-2	Sequence 2, Appl	c 821	10.2	53.7	27	2	US-08-609-443B-27	Sequence 27, Appl
749	10.2	53.7	24	3	US-09-216-430C-30	Sequence 30, Appl	822	10.2	53.7	27	2	US-08-467-034A-6	Sequence 6, Appl
750	10.2	53.7	24	3	US-09-439-423-15	Sequence 15, Appl	823	10.2	53.7	27	2	US-08-468-646A-6	Sequence 6, Appl
751	10.2	53.7	24	3	US-09-001-039B-1	Sequence 1, Appl	824	10.2	53.7	27	3	US-08-851-896-27	Sequence 27, Appl
752	10.2	53.7	24	3	US-09-735-271-1822	Sequence 1822, Ap	825	10.2	53.7	27	3	US-08-455-014B-6	Sequence 6, Appl
753	10.2	53.7	24	3			826	10.2	53.7	27	3		

827	10.2	53.7	27	3	US-08-471-645A-6	Sequence 6, Appli	900	10	52.6	19	5	US-09-543-679A-1515	Sequence 1515, Ap
828	10.2	53.7	27	3	US-09-428-082B-383	Sequence 383, App	c 901	10	52.6	20	2	US-08-149-105-6	Sequence 6, Appli
829	10.2	53.7	27	3	US-09-795-061-23	Sequence 23, Appl	c 902	10	52.6	20	2	US-08-317-847-6	Sequence 6, Appli
830	10.2	53.7	27	3	US-09-001-039B-9	Sequence 9, Appli	c 903	10	52.6	20	3	US-09-166-186-9	Sequence 9, Appli
831	10.2	53.7	27	4	US-09-856-725-6	Sequence 6, Appli	c 904	10	52.6	20	3	US-09-093-077-34	Sequence 34, Appli
832	10.2	53.7	28	2	US-08-362-670B-24	Sequence 24, Appl	c 905	10	52.6	20	3	US-09-313-932-9	Sequence 9, Appli
833	10.2	53.7	28	2	US-08-647-584-21	Sequence 21, Appli	c 906	10	52.6	20	3	US-09-313-932-430	Sequence 430, App
834	10.2	53.7	28	2	US-08-477-890-2	Sequence 2, Appli	c 907	10	52.6	20	3	US-09-428-583-13	Sequence 13, Appl
835	10.2	53.7	28	2	US-08-467-034A-2	Sequence 2, Appli	c 908	10	52.6	20	3	US-09-309-317-21	Sequence 21, Appl
836	10.2	53.7	28	3	US-08-333-576C-24	Sequence 24, Appli	c 909	10	52.6	20	3	US-09-404-056-4	Sequence 4, Appli
837	10.2	53.7	28	3	US-08-846-020A-2	Sequence 2, Appli	c 910	10	52.6	20	3	US-09-457-046B-38	Sequence 38, Appl
838	10.2	53.7	28	3	US-08-468-645A-2	Sequence 2, Appli	c 911	10	52.6	20	3	US-09-422-978-7954	Sequence 7954, Ap
839	10.2	53.7	28	3	US-08-808-324-24	Sequence 24, Appli	c 912	10	52.6	20	3	US-09-198-452A-2758	Sequence 2758, Ap
840	10.2	53.7	28	3	US-08-891-292A-94	Sequence 94, Appli	c 913	10	52.6	20	3	US-09-198-452A-4303	Sequence 4303, Ap
841	10.2	53.7	28	3	US-09-617-871-2	Sequence 2, Appli	c 914	10	52.6	20	3	US-09-940-244-187	Sequence 187, App
842	10.2	53.7	28	3	US-08-455-014B-2	Sequence 2, Appli	c 915	10	52.6	20	3	US-09-940-244-188	Sequence 188, App
843	10.2	53.7	28	3	US-08-471-645A-2	Sequence 2, Appli	c 916	10	52.6	20	3	US-09-940-244-189	Sequence 189, App
844	10.2	53.7	28	3	US-09-927-737C-94	Sequence 94, Appli	c 917	10	52.6	20	3	US-09-893-440-13	Sequence 13, Appli
845	10.2	53.7	28	3	US-09-732-615-24	Sequence 24, Appli	c 918	10	52.6	20	3	US-09-713-737-7	Sequence 7, Appli
846	10.2	53.7	28	3	US-09-945-182-24	Sequence 24, Appli	c 919	10	52.6	20	3	US-09-672-126B-127	Sequence 127, App
847	10.2	53.7	28	3	US-09-945-182-24	Sequence 24, Appli	c 920	10	52.6	20	3	US-09-672-126B-128	Sequence 128, App
848	10.2	53.7	28	3	US-10-273-051-24	Sequence 24, Appli	c 921	10	52.6	20	4	US-09-912-724-37	Sequence 37, Appl
849	10.2	53.7	28	3	US-09-001-039B-2	Sequence 2, Appli	c 922	10	52.6	20	5	US-09-670-105-34	Sequence 34, Appl
850	10.2	53.7	28	4	US-10-779-635-24	Sequence 24, Appl	c 923	10	52.6	20	5	US-09-543-679A-1278	Sequence 1278, Ap
851	10.2	53.7	29	2	US-08-647-584-45	Sequence 45, Appli	c 924	10	52.6	21	2	US-08-256-426B-282	Sequence 282, App
852	10.2	53.7	29	3	US-09-434-840-44	Sequence 44, Appli	c 925	10	52.6	21	2	US-08-437-607A-12	Sequence 12, Appl
853	10.2	53.7	30	2	US-08-802-547-14	Sequence 14, Appli	c 926	10	52.6	21	3	US-08-757-024-2	Sequence 2, Appli
854	10.2	53.7	30	2	US-08-678-039A-34	Sequence 34, Appli	c 927	10	52.6	21	3	US-08-472-663-59	Sequence 59, Appli
855	10.2	53.7	30	2	US-08-859-998-136	Sequence 136, App	c 928	10	52.6	21	3	US-09-103-663-59	Sequence 59, Appli
856	10.2	53.7	30	3	US-09-225-928-136	Sequence 136, App	c 929	10	52.6	21	3	US-09-245-159-7	Sequence 7, Appli
857	10.2	53.7	30	3	US-09-225-928-136	Sequence 136, App	c 930	10	52.6	21	3	US-09-380-836-58	Sequence 58, Appli
858	10.2	53.7	30	3	US-09-225-928-136	Sequence 136, App	c 931	10	52.6	21	3	US-09-382-552-168	Sequence 168, App
859	10.2	53.7	30	3	US-09-119-507B-54	Sequence 54, Appli	c 932	10	52.6	21	3	US-09-940-244-174	Sequence 174, App
860	10.2	53.7	30	3	US-08-897-556A-54	Sequence 54, Appli	c 933	10	52.6	21	3	US-09-940-244-181	Sequence 181, App
861	10.2	53.7	30	3	US-09-732-615-22	Sequence 22, Appli	c 934	10	52.6	21	3	US-09-940-244-186	Sequence 186, App
862	10.2	53.7	30	3	US-09-547-693-54	Sequence 54, Appli	c 935	10	52.6	21	3	US-09-657-472-1763	Sequence 1763, Ap
863	10.2	53.7	30	3	US-10-273-051-22	Sequence 22, Appli	c 936	10	52.6	21	3	US-10-071-411A-4	Sequence 4, Appli
864	10.2	53.7	30	5	US-09-780-929-114	Sequence 114, App	c 937	10	52.6	21	3	US-10-085-849-7	Sequence 7, Appli
865	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 938	10	52.6	21	3	US-09-093-972C-2	Sequence 2, Appli
866	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 939	10	52.6	21	3	US-09-875-453B-96	Sequence 96, Appl
867	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 940	10	52.6	21	3	US-09-381-212-186	Sequence 186, App
868	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 941	10	52.6	21	3	US-09-381-212-187	Sequence 187, App
869	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 942	10	52.6	21	3	US-09-381-212-188	Sequence 188, App
870	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 943	10	52.6	21	3	US-09-381-212-189	Sequence 189, App
871	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 944	10	52.6	21	3	US-09-713-601A-186	Sequence 186, App
872	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 945	10	52.6	21	3	US-09-713-601A-187	Sequence 187, App
873	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 946	10	52.6	21	3	US-09-713-601A-188	Sequence 188, App
874	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 947	10	52.6	21	3	US-09-713-601A-189	Sequence 189, App
875	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 948	10	52.6	21	5	US-09-543-679A-2	Sequence 2, Appli
876	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 949	10	52.6	22	3	US-08-660-645A-37	Sequence 37, Appl
877	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 950	10	52.6	22	3	US-09-298-718-37	Sequence 37, Appl
878	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 951	10	52.6	22	3	US-09-546-969-37	Sequence 37, Appl
879	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 952	10	52.6	22	3	US-08-980-832-16	Sequence 16, Appl
880	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 953	10	52.6	22	3	US-09-547-267-37	Sequence 37, Appl
881	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 954	10	52.6	22	3	US-09-920-923B-16	Sequence 16, Appl
882	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 955	10	52.6	22	3	US-09-940-244-182	Sequence 182, App
883	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 956	10	52.6	22	3	US-09-381-212-174	Sequence 174, App
884	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 957	10	52.6	22	3	US-09-381-212-181	Sequence 181, App
885	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 958	10	52.6	22	3	US-09-713-601A-174	Sequence 174, App
886	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 959	10	52.6	22	3	US-08-577-858A-22	Sequence 22, Appl
887	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 960	10	52.6	23	2	US-08-577-858A-22	Sequence 22, Appl
888	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 961	10	52.6	23	3	US-08-577-858A-22	Sequence 22, Appl
889	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 962	10	52.6	23	3	US-09-245-041-97	Sequence 97, Appl
890	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 963	10	52.6	23	3	US-09-358-055B-98	Sequence 98, Appl
891	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 964	10	52.6	23	3	US-09-893-238-97	Sequence 97, Appl
892	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 965	10	52.6	23	3	US-09-856-662-98	Sequence 98, Appl
893	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 966	10	52.6	23	3	US-09-381-212-182	Sequence 182, App
894	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 967	10	52.6	23	3	US-09-713-601A-182	Sequence 182, App
895	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 968	10	52.6	24	2	US-07-974-447-1	Sequence 1, Appli
896	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 969	10	52.6	24	2	US-07-974-447-1	Sequence 1, Appli
897	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 970	10	52.6	24	2	US-08-149-199-1	Sequence 1, Appli
898	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 971	10	52.6	24	2	US-08-149-199-1	Sequence 1, Appli
899	10.2	53.7	30	5	US-09-854-867-543	Sequence 543, App	c 972	10	52.6	24	2	US-08-381-592-7	Sequence 7, Appli

C 973 10 52.6 24 2 US-08-592-820-13 Sequence 13, Appl
C 974 10 52.6 24 2 US-08-858-767-1 Sequence 1, Appl
C 975 10 52.6 24 2 US-08-858-767-3 Sequence 3, Appl
C 976 10 52.6 24 2 US-08-863-028-1 Sequence 1, Appl
C 977 10 52.6 24 2 US-08-863-028-3 Sequence 3, Appl
C 978 10 52.6 24 2 US-08-547-214-1 Sequence 1, Appl
C 979 10 52.6 24 2 US-08-547-214-15 Sequence 15, Appl
C 980 10 52.6 24 2 US-08-761-277A-59 Sequence 59, Appl
C 981 10 52.6 24 2 US-08-663-823B-1 Sequence 1, Appl
C 982 10 52.6 24 2 US-08-663-823B-15 Sequence 15, Appl
C 983 10 52.6 24 2 US-08-663-823B-60 Sequence 60, Appl
C 984 10 52.6 24 2 US-08-663-823B-62 Sequence 62, Appl
C 985 10 52.6 24 2 US-08-993-118-11 Sequence 11, Appl
C 986 10 52.6 24 3 US-08-748-130-23 Sequence 23, Appl
C 987 10 52.6 24 3 US-08-392-794A-13 Sequence 13, Appl
C 988 10 52.6 24 3 US-08-845-528C-11 Sequence 11, Appl
C 989 10 52.6 24 3 US-08-874-825-27 Sequence 27, Appl
C 990 10 52.6 24 3 US-08-874-825-29 Sequence 29, Appl
C 991 10 52.6 24 3 US-08-874-825-31 Sequence 31, Appl
C 992 10 52.6 24 3 US-08-874-825-33 Sequence 33, Appl
C 993 10 52.6 24 3 US-08-874-825-53 Sequence 53, Appl
C 994 10 52.6 24 3 US-08-874-825-67 Sequence 67, Appl
C 995 10 52.6 24 3 US-08-874-825-107 Sequence 107, App
C 996 10 52.6 24 3 US-08-874-825-109 Sequence 109, App
C 997 10 52.6 24 3 US-08-663-824-27 Sequence 27, Appl
C 998 10 52.6 24 3 US-08-663-824-29 Sequence 29, Appl
C 999 10 52.6 24 3 US-08-663-824-31 Sequence 31, Appl
C1000 10 52.6 24 3 US-08-663-824-33 Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-914-961-8/c
; Sequence 8, Application US/08914961
; Patent No. 6018042
; GENERAL INFORMATION:
; APPLICANT: Mett, Helmut
; APPLICANT: Hanert, Robert
; APPLICANT: Dean, Nicholas Mark
; TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914, 961
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,753
; FILING DATE: 09-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprull, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-20047/P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; POSITION IN GENOME:
; MAP POSITION: 1046
; UNITS: bp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..20
; OTHER INFORMATION: /note= "All nucleotides are of the
; US-08-914-961-8 phosphorothioate type"

Query Match 72.6%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGTGCT 19
Db 19 AGAAGGTGGTGATGCT 3
||||| ||||| |||||
||||| ||||| |||||

RESULT 2
US-10-085-612A-23/c
; Sequence 23, Application US/10085612A
; Patent No. 6929912
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Hall, Jeff
; APPLICANT: Petros, William
; APPLICANT: Colvin, Oliver
; APPLICANT: Vredenburgh, James
; APPLICANT: Marks, Jeffrey
; TITLE OF INVENTION: METHODS FOR EVALUATING THE ABILITY TO METABOLIZE PHARMACEUTICALS
; FILE REFERENCE: DNA-5-C1
; CURRENT APPLICATION NUMBER: US/10/085,612A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/144,367
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/271,630
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-085-612A-23

Query Match 70.5%; Score 13.4; DB 3; Length 22;
Best Local Similarity 93.3%; Pred. No. 5.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGTGGG 15
Db 22 GGAGAGGAGGTGGG 8
||||| ||||| |||||
||||| ||||| |||||

RESULT 3
US-09-422-978-9827/c
; Sequence 9827, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/067,626
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,688
; FILING DATE: 06-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/491
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-067-626-12

Query Match 69.5%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred.No.6.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels

QY 1 GGAGAGGGGGTGGGTGC 18
    ||| ||| ||| ||| |||
Db 1 GGGGATGGCGGTGGGTGC 18

RESULT 6
US-08-173-489C-359/c
; Sequence 359, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959

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; INFORMATION FOR SEQ ID NO: 359:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: p53 gene, nucleotides 1427-1453
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Harlow, E, Williamson, N M, Ralston, R,
;          Helfman, D M, Adams T E.
; TITLE: Molecular cloning and in
;        vitro expression of a cDNA for human cellular
;        tumor antigen p53
; JOURNAL: Molecular and Cellular Biology
; VOLUME: 5
; PAGES: 1601-1610
; DATE: 1985
; RELEVANT RESIDUES IN SEQ ID NO: 359 :FROM 1 TO 27
US-08-173-489C-359

Query Match          67.4%; Score 12.8; DB 2; Length 27;
Best Local Similarity 87.5%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTG 17
Db      17 GAGATGGGGTGGGAG 2

RESULT 7
US-08-943-731-424
; Sequence 424, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KOKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; STREET: FLR
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 424:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-424

Query Match          66.3%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGGTGCT 19
Db      3 GGAAATGAGGTGGTGCT 21

RESULT 8
US-09-282-146-4/c
; Sequence 4, Application US/09282146A
; Patent No. 6303847
; GENERAL INFORMATION:
; APPLICANT: KAWAKAKI, Akiyoshi
; APPLICANT: EBINUMA, Hiroyasu
; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
; TITLE OF INVENTION: BIOSYNTHESIS PATHWAY
; FILE REFERENCE: 4859-0027-0
; CURRENT APPLICATION NUMBER: US/09/282,146A
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: JP 10-125171
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
US-09-282-146-4

Query Match          65.3%; Score 12.4; DB 3; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GAAGGGGGTGGGTG 17
Db      17 GAAGGGGGTGGTG 4

RESULT 9
US-09-205-921-33
; Sequence 33, Application US/09205921A
; Patent No. 6008048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
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, STREET: P.O. Box 4433
, CITY: Houston
, STATE: Texas
, COUNTRY: USA
, ZIP: 77210
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, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/927,219
, FILING DATE: Concurrently Herewith
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 60/029,679
, FILING DATE: 30-OCT-1996
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 60/028,056
, FILING DATE: 02-OCT-1996
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 60/025,719
, FILING DATE: 10-SEP-1996
, ATTORNEY/AGENT INFORMATION:
, NAME: Wilson, Mark B.
, REGISTRATION NUMBER: 37,259
, REFERENCE/DOCKET NUMBER: ARCD:272
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 512/418-3000
, TELEFAX: 512/474-7577
, INFORMATION FOR SEQ ID NO: 64:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 22 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
,
, US-08-927-219-64
,
, Query Match 65.3%; Score 12.4; DB 3;
, Best Local Similarity 92.9%; Pred. No. 1.5e+04;
, Matches 13; Conservative 0; Mismatches 1;
,
, Qy 1 GGAGAGGGGGTGG 14
, |||||
, Db 14 GGAGTAGGGGGTGG 1
,
, RESULT 12
, US-09-716-964B-191/c
, Sequence 191, Application US/09716964B
, Patent No. 6897053
, GENERAL INFORMATION:
, APPLICANT: O'Donnell, Michael E.
, APPLICANT: Yuzhakov, Alexander
, APPLICANT: Yurteva, Olga
, APPLICANT: Jeruzalmi, David
, APPLICANT: Bruck, Irina
, APPLICANT: Kuriyan, John
, TITLE OF INVENTION: ENZYMS DERIVED FROM THERMOPHILIC
, TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICATOR
, TITLE OF INVENTION: USE THEREOF
, FILE REFERENCE: 22221/1030
, CURRENT APPLICATION NUMBER: US/09/716,964B
, CURRENT FILING DATE: 2000-11-21
, PRIOR APPLICATION NUMBER: 60/143,202
, PRIOR FILING DATE: 1997-04-08
, PRIOR APPLICATION NUMBER: 08/823,407
, PRIOR FILING DATE: 1997-04-08
, PRIOR APPLICATION NUMBER: 09/057,416
, PRIOR FILING DATE: 1998-04-08
, NUMBER OF SEQ ID NOS: 212
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 191

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; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-716-964B-191

Query Match      65.3%; Score 12.4; DB 3; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      19 GGAGAGGGTGGTGG 6

RESULT 13
US-08-504-511A-6/c
; Sequence 6, Application US/08504511A
; Patent No. 5561224
; GENERAL INFORMATION:
; APPLICANT: Rosenfeld, M. G.
; APPLICANT: Andersen, B.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR THE REGULATION
; TITLE OF INVENTION: OF THE DEVELOPMENT OF SKIN AND HAIR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,511A
; FILING DATE: 20-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Howells, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: Skn-11 POU
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..30
US-08-504-511A-6

Query Match      65.3%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      24 GGAGAGGAGGGTGG 11
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RESULT 14
US-09-119-507B-10/c
; Sequence 10, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-10

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      29 GGAGATGGGGGTGG 16

RESULT 15
US-09-119-507B-38/c
; Sequence 38, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-38

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGG 14
Db      29 GGAGATGGGGGTGG 16

RESULT 16
US-09-119-507B-39
; Sequence 39, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
```



```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-39

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 11 GGAGATGGGGTGG 24

RESULT 17
US-08-897-556A-10/c
; Sequence 10, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-897-556A-10

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 29 GGAGATGGGGTGG 16

RESULT 18
US-08-897-556A-38/c
; Sequence 38, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
```

```
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-897-556A-38

Query Match      65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGG 14
    ||||| |||||
Db 29 GGAGATGGGGTGG 16

RESULT 19
US-08-897-556A-39
; Sequence 39, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-897-556A-39

Query Match 65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
|||||
Db 11 GGAGATGGGGTGG 24

RESULT 20

US-09-547-693-10/c
Sequence 10, Application US/09547693
Patent No. 6639050

GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
US-09-547-693-10

Query Match 65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
|||||
Db 29 GGAGATGGGGTGG 16

RESULT 21

US-09-547-693-38/c
Sequence 38, Application US/09547693
Patent No. 6639050

GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 38
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
US-09-547-693-38

Query Match 65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
|||||
Db 29 GGAGATGGGGTGG 16

RESULT 22

US-09-547-693-39
Sequence 39, Application US/09547693
Patent No. 6639050

GENERAL INFORMATION:

APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION: Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial/Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Synthetic
US-09-547-693-39

Query Match 65.3%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGG 14
|||||
Db 11 GGAGATGGGGTGG 24

RESULT 23

US-08-531-556-122/c
Sequence 122, Application US/08531556
Patent No. 5776682

GENERAL INFORMATION:

APPLICANT: Agoulrik, Alexander I
APPLICANT: Kent First, Marijo
APPLICANT: Muallem, Ariege
TITLE OF INVENTION: MALE INFERTILITY Y-DELETION DETECTION
TITLE OF INVENTION: BATTERY
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,556
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sara Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506.034CIP
TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-531-556-122

Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 24

US-08-690-734A-81/c
Sequence 81, Application US/08690734A
Patent No. 5871920

GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
TITLE OF INVENTION: DAZ: A GENE ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,734A
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-07A
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-690-734A-81

Query Match 64.2%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 25

US-08-742-185-81/c
Sequence 81, Application US/08742185
Patent No. 6020476
GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-07A2
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-742-185-81

Query Match 64.2%; Score 12.2; DB 3; Length 18;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGTG 17
Db 18 GAAGAAGGGGGATGGTG 2

RESULT 26

US-08-448-386A-10/c
Sequence 10, Application US/08448386A
Patent No. 5840708

GENERAL INFORMATION:
APPLICANT: START Technology, Partnership
TITLE OF INVENTION: Administration of Oligonucleotides
TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and
TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
TITLE OF INVENTION: Nervous System
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA

COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,386A
FILING DATE: 14-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,582
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-448-386A-10

Query Match 64.2%; Score 12.2; DB 2; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
||||| ||||| |||||
Db 17 GGAGATGGAGGTAGTG 1

RESULT 27
US-08-816-426-10/c
Sequence 10, Application US/08816426
Patent No. 6025193
GENERAL INFORMATION:
APPLICANT: START Technology, Partnership
TITLE OF INVENTION: Administration of Oligonucleotides
TITLE OF INVENTION: Antisense to Dopamine Receptor mRNA for Diagnosis and
TITLE OF INVENTION: Treatment of Pathological Conditions of the Dopaminergic
TITLE OF INVENTION: Nervous System
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,426
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/448,386
FILING DATE:
APPLICATION NUMBER: US 07/991,582
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-816-426-10

Query Match 64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
||||| ||||| |||||
Db 17 GGAGATGGAGGTAGTG 1

RESULT 28
US-08-943-731-533/c
Sequence 533, Application US/08943731
Patent No. 6265157
GENERAL INFORMATION:
APPLICANT: PROCKOP, DARWIN J.
APPLICANT: SPOTILA, LORETTA D.
APPLICANT: DELTAS, CONSTANTINOS D.
APPLICANT: SEREDA, LARISA
APPLICANT: LARSON, ANDREA W.
APPLICANT: PACK, MICHAEL
APPLICANT: COLIGE, ALAIN
APPLICANT: EARLY, JAMES
APPLICANT: KORKKO, JARMO
APPLICANT: ALA-KOKKO, LEENA, et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
NUMBER OF SEQUENCES: 666
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
CITY: PHILADELPHIA
STATE: PA
COUNTRY: USA
ZIP: 19103-7086
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,731
FILING DATE: 03-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,322
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/803,628
FILING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991

```
;
;
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 533:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-533

Query Match      64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
Db 17 GGAGATGGGGTGTCTG 1

RESULT 29
US-08-943-731-534
; Sequence 534, Application US/08943731
; Patent No. 6265157
; GENERAL INFORMATION:
; APPLICANT: PROCKOP, DARWIN J.
; APPLICANT: SPOTILA, LORETTA D.
; APPLICANT: DELTAS, CONSTANTINOS D.
; APPLICANT: SEREDA, LARISA
; APPLICANT: LARSON, ANDREA W.
; APPLICANT: PACK, MICHAEL
; APPLICANT: COLIGE, ALAIN
; APPLICANT: EARLY, JAMES
; APPLICANT: KORKKO, JARMO
; APPLICANT: ALA-KORKKO, LEENA, et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
; NUMBER OF SEQUENCES: 666
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,731
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,322
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/803,628
; FILING DATE: 03-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9598-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; TELEX: 831-494
; INFORMATION FOR SEQ ID NO: 534:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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```
;
;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-943-731-534

Query Match      64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
Db 4 GGAGATGGGGTGTCTG 20

RESULT 30
US-09-198-452A-6511/c
; Sequence 6511, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6511
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-6511

Query Match      64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAAGGGGGTGGGTGC 18
Db 19 GAGAAGGGGTAGGAGC 3

RESULT 31
US-09-865-879-29/c
; Sequence 29, Application US/09865879
; Patent No. 6767705
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Dokmanovic, Milos
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF RETINOIDS
; TITLE OF INVENTION: REGULATED BY RETINOIDS
; FILE REFERENCE: 99,216-H
; CURRENT APPLICATION NUMBER: US/09/865,879
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense primer for P28 alpha
US-09-865-879-29

Query Match      64.2%; Score 12.2; DB 3; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
Db 1 GGAGATGGGGTGTCTG 1
```

Db 19 GAAGAAGGGGAGGATG 3

RESULT 32

PCT-US93-12161-10/c
 ; Sequence 10, Application PC/TUS9312161
 ; GENERAL INFORMATION:
 ; APPLICANT: START Technology Partnership
 ; TITLE OF INVENTION: Administration of
 ; TITLE OF INVENTION: Oligonucleotides Antisense to Dopamine Receptor
 ; TITLE OF INVENTION: mRNA for Diagnosis and Treatment of Pathological
 ; TITLE OF INVENTION: Conditions of the Dopaminergic Nervous System
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and
 ; ADDRESSEE: Skillman
 ; STREET: 1601 Market Street, Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version
 ; SOFTWARE: #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/12161
 ; FILING DATE: 14-DEC-1993
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/991,582
 ; FILING DATE: 14-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reed, Janet E.
 ; REGISTRATION NUMBER: 36,252
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 563-4100
 ; TELEFAX: (215) 563-4044
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: YES
 PCT-US93-12161-10

Query Match 64.2%; Score 12.2; DB 7; Length 20;
 Best Local Similarity 82.4%; Pred. No. 1.8e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGAGAAGGGGTGGGTG 17
 Db 17 GGAGATGGAGGTAGGTG 1

RESULT 33

US-10-118-079-12/c
 ; Sequence 12, Application US/10118079
 ; Patent No. 6855688
 ; GENERAL INFORMATION:
 ; APPLICANT: MCKERRACHER, LISA
 ; TITLE OF INVENTION: FUSION PROTEINS
 ; FILE REFERENCE: 06746-004-US-03
 ; CURRENT APPLICATION NUMBER: US/10/118,079
 ; CURRENT FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: CA 2,367,636
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: CA 2,362,004

; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: CA 2,342,970
 ; PRIOR FILING DATE: 2001-04-12
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide used in the amplification of a sequence corresponding
 ; OTHER INFORMATION: ing to amino acid 27-72 of HIV-1 Tat
 US-10-118-079-12

Query Match 64.2%; Score 12.2; DB 3; Length 21;
 Best Local Similarity 82.4%; Pred. No. 1.8e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGAAGGGGTGGGTGCT 19
 Db 17 AGAAGGTGGTGGCTGT 1

RESULT 34

US-08-330-123A-6/c
 ; Sequence 6, Application US/08330123A
 ; Patent No. 5583016
 ; GENERAL INFORMATION:
 ; APPLICANT: VILLEPONTREAU, Bryant
 ; APPLICANT: FENG, Junli
 ; APPLICANT: FUNK, Walter
 ; APPLICANT: ANDREWS, William H.
 ; TITLE OF INVENTION: HUMAN TELOMERASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/330,123A
 ; FILING DATE: 27-OCT-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/272,102
 ; FILING DATE: 07-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15389-000810
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA
 US-08-330-123A-6

Query Match 64.2%; Score 12.2; DB 2; Length 22;
 Best Local Similarity 82.4%; Pred. No. 1.8e+04;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGC 18
||||| ||| ||| |||
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 35
US-08-660-678A-28/c
; Sequence 28, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-28

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGC 18
||||| ||| ||| |||
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 36
US-08-485-778-8/c
; Sequence 8, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-778-8

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGC 18
||||| ||| ||| |||
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 37
US-08-472-802C-43/c
; Sequence 43, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-472-802C-43

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
DB 18 GAGAGGGCGTAGGCG 2

RESULT 38
US-09-068-109-3
Sequence 3, Application US/09068109
Patent No. 5986172
GENERAL INFORMATION:
APPLICANT: UCHIMIYA, HIROFUMI
APPLICANT: FUSHIMI, TAKAOMI
APPLICANT: KUDOU, UWE
APPLICANT: TAGAWA, MICHITO
TITLE OF INVENTION: RICE NADH-DEPENDENT REDUCTASE, GENE THEREFOR AND USE
FILE REFERENCE: 0049-0250-0 PCT
CURRENT APPLICATION NUMBER: US/09/068,109
CURRENT FILING DATE: 1998-05-05
EARLIER APPLICATION NUMBER: PCT/JP95/02641
EARLIER FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Oligomer
US-09-068-109-3

Query Match 64.2%; Score 12.2; DB 2; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAGGGGGTGGTGC 19
|||||
DB 1 AGTACGGGGTGGTGC 17

RESULT 39
US-08-520-550A-8/c
Sequence 8, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millicia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-8

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGC 18
|||||
DB 18 GAGAGGGCGTAGGCG 2

RESULT 40
US-08-998-443-28/c
Sequence 28, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase

;/ NUMBER OF SEQUENCES: 30
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, Eighth Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94111-3834
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/998,443
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/660,678
;/ FILING DATE: 05-JUN-1996
;/ APPLICATION NUMBER: US/08/330,123
;/ FILING DATE: 27-OCT-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/272,102
;/ FILING DATE: 07-JUL-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Storella, John R.
;/ REGISTRATION NUMBER: 32,944
;/ REFERENCE/DOCKET NUMBER: 015389-000811US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 28:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 22 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA
;/ US-08-998-443-28

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTGC 18
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 41
US-09-580-517-6/c
;/ Sequence 6, Application US/09580517
;/ Patent No. 6320039
;/ GENERAL INFORMATION:
;/ APPLICANT: VILLEPONTAU, Bryant
;/ FENG, Junli
;/ FUNK, Walter
;/ ANDREWS, William H.
;/ TITLE OF INVENTION: HUMAN TELOMERASE
;/ NUMBER OF SEQUENCES: 25
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend Kourie and Crew
;/ STREET: 379 Lytton Avenue
;/ CITY: Palo Alto
;/ STATE: California
;/ COUNTRY: US
;/ ZIP: 94301
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/580,517
;/ FILING DATE: 25-May-2000
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/330,123
;/ FILING DATE: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Smith, William M
;/ REGISTRATION NUMBER: 30,223
;/ REFERENCE/DOCKET NUMBER: 15389-000810
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 326-2400
;/ TELEFAX: (415) 326-2422
;/ INFORMATION FOR SEQ ID NO: 6:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 22 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: RNA
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;/ US-09-580-517-6

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGGTGC 18
Db 18 GAGAGGGGGTGGGTGC 2

RESULT 42
US-09-057-351-42/c
;/ Sequence 42, Application US/09057351
;/ Patent No. 6548298
;/ GENERAL INFORMATION:
;/ APPLICANT: Villeponteau, Bryant
;/ APPLICANT: Feng, Junli
;/ APPLICANT: Funk, Walter
;/ APPLICANT: Andrews, William H.
;/ TITLE OF INVENTION: Mammalian Telomerase
;/ NUMBER OF SEQUENCES: 42
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, Eighth Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94111-3834
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/057,351
;/ FILING DATE: 08-APR-1994
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/272,102
;/ FILING DATE: 07-JUL-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/330,123
;/ FILING DATE: 27-OCT-1994
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/472,802
;/ FILING DATE: 07-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Storella, John R.
;/ REGISTRATION NUMBER: 32,944
;/ REFERENCE/DOCKET NUMBER: 015389-000821US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-09-057-351-42

Query Match 64.2%; Score 12.2; DB 3; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTGC 18
|||||
DB 18 GAGAGGGCGTAGGC 2

RESULT 43
US-09-980A-2
Sequence 2, Application US/09070980A
Patent No. 6110725
GENERAL INFORMATION:
APPLICANT: DELLEY, MICHELE
APPLICANT: GERMOND, JACQUES
APPLICANT: LAPIERRE, LUCIANE
APPLICANT: MOLLET, BEAT
APPLICANT: PRIDMORE, RAYMOND
TITLE OF INVENTION: PRODUCTION OF L(+)-LACTATE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: VOGT&O'DONNELL, LLP
STREET: 707 WESTCHESTER AVENUE
CITY: WHITE PLAINES
STATE: NEW YORK
COUNTRY: USA
ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,980A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97201337.9
FILING DATE: 03-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: PLAUTZ, DAVID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328 00 55
TELEFAX: (914) 328 00 60
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-070-980A-2

Query Match 64.2%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17
|||||
DB 6 GTAGAAGGGCGGTGTG 22

RESULT 44
US-09-490-217-2
Sequence 2, Application US/09490217
Patent No. 6258587
GENERAL INFORMATION:
APPLICANT: DELLEY, MICHELE
APPLICANT: GERMOND, JACQUES
APPLICANT: LAPIERRE, LUCIANE
APPLICANT: MOLLET, BEAT
APPLICANT: PRIDMORE, RAYMOND
TITLE OF INVENTION: PRODUCTION OF L(+)-LACTATE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: VOGT&O'DONNELL, LLP
STREET: 707 WESTCHESTER AVENUE
CITY: WHITE PLAINES
STATE: NEW YORK
COUNTRY: USA
ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,217
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/070,980
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PLAUTZ, DAVID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328 00 55
TELEFAX: (914) 328 00 60
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-490-217-2

Query Match 64.2%; Score 12.2; DB 3; Length 23;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTG 17
|||||
DB 6 GTAGAAGGGCGGTGTG 22

RESULT 45
US-08-729-598-7
Sequence 7, Application US/08729598
Patent No. 6001657
GENERAL INFORMATION:
APPLICANT: Hardin, Charles C.
APPLICANT: Brown II, Bernard A.
APPLICANT: Roberts, John J.
TITLE OF INVENTION: Antibodies That Selectively Bind
TITLE OF INVENTION: Quadruplex Nucleic Acids
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sorojini J. Biswas
STREET: P.O. Box 37428
CITY: Raleigh
STATE: No. 6001657th Carolina

;; COUNTRY: USA
;; ZIP: 27627
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,598
;; FILING DATE: 11-OCT-1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Biswas, Sorojini J.
;; REGISTRATION NUMBER: 39,111
;; REFERENCE/DOCKET NUMBER: 5051-301A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 854-1400
;; TELEFAX: (919) 854-1401
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: DNA (genomic)
US-08-729-598-7

Query Match 64.2%; Score 12.2; DB 3; Length 24;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
||||| ||||| |||||
Db 7 GGAGAGGGGGGAGGGGG 23

RESULT 46
US-08-802-547-2
; Sequence 2, Application US/0802547
; Patent No. 5780611
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT EXPRESSION OF
; TITLE OF INVENTION: COLLAGEN GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: MO USA
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,547
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 24129-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816-474-9050
; TELEFAX: 816-474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 26 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; POSITION IN GENOME:
;; UNITS: bp
US-08-802-547-2

Query Match 64.2%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
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Db 8 GGGGAGGGGGCTGGGTG 24

RESULT 47
US-08-712-357-2
; Sequence 2, Application US/08712357
; Patent No. 5808037
; GENERAL INFORMATION:
; APPLICANT: Guntaka, Ramareddy V.
; APPLICANT: Weber, Karl T.
; APPLICANT: Kovacs, Attila
; APPLICANT: Kandala, Jagannadhachari
; TITLE OF INVENTION: OLIGOMERS WHICH INHIBIT
; TITLE OF INVENTION: EXPRESSION OF COLLAGEN GENES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,357
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; POSITION IN GENOME:
; UNITS: bp
US-08-712-357-2

Query Match 64.2%; Score 12.2; DB 2; Length 26;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTG 17
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Db      8 GGGGAGGGGGCTGGGTG 24

RESULT 48
US-09-460-555-4/c
; Sequence 4, Application US/09460555
; Patent No. 6563014
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: Goldstein, Harris
; APPLICANT: Paul, Jessie B.
; TITLE OF INVENTION: SELF-CONTAINED SYSTEM FOR SUSTAINED VIRAL REPLICATION
; FILE REFERENCE: 96700/552
; CURRENT APPLICATION NUMBER: US/09/460,555
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-460-555-4

Query Match      64.2%; Score 12.2; DB 3; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      22 GGAGAGGGCGGTGGG 6

RESULT 49
US-09-304-232-866
; Sequence 866, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 866
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TBXASEX11 105
US-09-304-232-866

Query Match      64.2%; Score 12.2; DB 3; Length 29;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GAGAGGGGGTGGGTGC 18
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Db      7 GAGATGCCYGTGGGTGC 23

RESULT 50
US-09-685-256-10
; Sequence 10, Application US/09685256
; Patent No. 6660904
; GENERAL INFORMATION:
; APPLICANT: Bryant, Joseph L.
; TITLE OF INVENTION: HIV AND CD4 TRANSGENIC ANIMALS AND USES THEREFOR
; FILE REFERENCE: 4115-150 CIP
; CURRENT APPLICATION NUMBER: US/09/685,256
; CURRENT FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-685-256-10

Query Match      64.2%; Score 12.2; DB 3; Length 30;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGGTGGGTG 17
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Db      12 GGAGAGGGCGGTGGG 28

Search completed: October 14, 2006, 19:43:11
Job time : 117 secs
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GenCore version 5.1.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:43:30 ; Search time 809 Seconds
(without alignments)
288.585 Million cell updates/sec

Title: US-10-604-926A-4539

Perfect score: 19

Sequence: 1 ggagaggggggtggtgct 19

Scoring table: IDENTITY NUC

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Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 23237482

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Maximum DB seq length: 30

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	18	94.7	23	US-10-310-914A-148966	Sequence 148966, A
c	5	18	94.7	23	US-10-310-914A-1065883	Sequence 1065883, A
c	6	16	84.2	19	US-10-310-914A-148924	Sequence 148924, A
7	15.8	83.2	19	11	US-10-310-914A-129493	Sequence 129493, A
8	15.8	83.2	19	11	US-10-310-914A-572030	Sequence 572030, A
c	9	15.8	83.2	22	US-10-310-914A-910792	Sequence 910792, A
c	10	15.8	83.2	23	US-10-310-914A-129473	Sequence 129473, A
c	11	15.8	83.2	23	US-10-310-914A-203215	Sequence 203215, A
c	12	15.8	83.2	24	US-10-310-914A-203187	Sequence 203187, A
c	13	15.4	81.1	18	US-10-310-914A-869326	Sequence 869326, A
c	14	15	78.9	18	US-10-310-914A-1065866	Sequence 1065866, A
c	15	15	78.9	22	US-10-310-914A-148939	Sequence 148939, A
c	16	15	78.9	22	US-10-310-914A-1065867	Sequence 1065867, A
c	17	14.8	77.9	19	US-10-310-914A-203240	Sequence 203240, A

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Sequence 203210, A	20	11	US-10-310-914A-203210
Sequence 232190, A	21	11	US-10-310-914A-232190
Sequence 910812, A	22	11	US-10-310-914A-910812
Sequence 184336, A	25	13	US-11-060-756-184336
Sequence 223194, A	25	13	US-11-060-756-223194
Sequence 233127, A	25	13	US-11-060-756-233127
Sequence 296887, A	25	13	US-11-060-756-296887
Sequence 302280, A	25	13	US-11-060-756-302280
Sequence 491217, A	18	11	US-10-310-914A-491217
Sequence 492205, A	19	11	US-10-310-914A-492205
Sequence 491213, A	19	11	US-10-310-914A-491213
Sequence 910789, A	19	11	US-10-310-914A-910789
Sequence 910790, A	19	11	US-10-310-914A-910790
Sequence 289813, A	20	11	US-10-310-914A-289813
Sequence 455081, A	24	11	US-10-310-914A-455081
Sequence 856024, A	24	11	US-10-310-914A-856024
Sequence 986078, A	24	11	US-10-310-914A-986078
Sequence 939254, A	19	11	US-10-310-914A-939254
Sequence 1039501, A	19	11	US-10-310-914A-1039501
Sequence 1039502, A	19	11	US-10-310-914A-1039502
Sequence 1051671, A	19	11	US-10-310-914A-1051671
Sequence 1114392, A	19	11	US-10-310-914A-1114392
Sequence 1151400, A	19	11	US-10-310-914A-1151400
Sequence 649973, A	20	11	US-10-310-914A-649973
Sequence 1207983, A	20	11	US-10-310-914A-1207983
Sequence 112107, A	22	11	US-10-310-914A-112107
Sequence 35504, A	25	15	US-11-121-849-35504
Sequence 27, Appl	26	7	US-10-120-637A-27
Sequence 27, Appl	26	9	US-10-913-271-27
Sequence 27, Appl	26	9	US-10-913-226-27
Sequence 479763, A	26	9	US-10-913-779-27
Sequence 148931, A	30	16	US-11-151-227-7
Sequence 165859, A	21	11	US-10-310-914A-148931
Sequence 538065, A	18	11	US-10-310-914A-538065
Sequence 538107, A	18	11	US-10-310-914A-538107
Sequence 571613, A	18	11	US-10-310-914A-571613
Sequence 571614, A	18	11	US-10-310-914A-571614
Sequence 571973, A	18	11	US-10-310-914A-571973
Sequence 577734, A	18	11	US-10-310-914A-577734
Sequence 811281, A	19	11	US-10-310-914A-811281
Sequence 811768, A	19	11	US-10-310-914A-811768
Sequence 936239, A	19	11	US-10-310-914A-936239
Sequence 936240, A	19	11	US-10-310-914A-936240
Sequence 486427, A	19	14	US-11-083-784-486427
Sequence 487290, A	19	14	US-11-083-784-487290
Sequence 487361, A	19	14	US-11-083-784-487361
Sequence 486427, A	19	15	US-11-101-244-486427
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Sequence 482322, A	20	11	US-10-310-914A-482322
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Sequence 295842, A	21	11	US-10-310-914A-295842
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Sequence 296260, A	21	11	US-10-310-914A-296260
Sequence 296352, A	21	11	US-10-310-914A-296352
Sequence 296416, A	21	11	US-10-310-914A-296416
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Sequence 296892, A	21	11	US-10-310-914A-296892

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92	13.8	72.6	21	11	US-10-310-914A-297204	Sequence 297204,	165	13.8	72.6	27	11	US-10-310-914A-295910	Sequence 295910,
93	13.8	72.6	21	11	US-10-310-914A-297546	Sequence 297546,	166	13.8	72.6	27	11	US-10-310-914A-296086	Sequence 296086,
94	13.8	72.6	21	11	US-10-310-914A-297805	Sequence 297805,	167	13.8	72.6	27	11	US-10-310-914A-296264	Sequence 296264,
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c 100	13.8	72.6	21	11	US-10-310-914A-1052388	Sequence 1052388,	173	13.8	72.6	27	11	US-10-310-914A-297552	Sequence 297552,
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102	13.8	72.6	22	11	US-10-310-914A-273344	Sequence 273344,	c 175	13.8	72.6	27	11	US-10-310-914A-297872	Sequence 297872,
103	13.8	72.6	22	11	US-10-310-914A-294376	Sequence 294376,	c 176	13.8	72.6	27	11	US-10-310-914A-705013	Sequence 705013,
104	13.8	72.6	22	11	US-10-310-914A-294702	Sequence 294702,	c 177	13.8	72.6	28	11	US-10-310-914A-369026	Sequence 369026,
105	13.8	72.6	22	11	US-10-310-914A-294903	Sequence 294903,	c 178	13.8	72.6	28	11	US-10-310-914A-901220	Sequence 901220,
106	13.8	72.6	22	11	US-10-310-914A-295071	Sequence 295071,	179	13.4	70.5	18	11	US-10-310-914A-73962	Sequence 73962, A
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108	13.8	72.6	22	11	US-10-310-914A-295390	Sequence 295390,	c 181	13.4	70.5	18	11	US-10-310-914A-192896	Sequence 192896,
109	13.8	72.6	22	11	US-10-310-914A-295544	Sequence 295544,	c 182	13.4	70.5	18	11	US-10-310-914A-434402	Sequence 434402,
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111	13.8	72.6	22	11	US-10-310-914A-296204	Sequence 296204,	184	13.4	70.5	18	11	US-10-310-914A-1039438	Sequence 1039438,
112	13.8	72.6	22	11	US-10-310-914A-296520	Sequence 296520,	185	13.4	70.5	18	11	US-10-310-914A-1216963	Sequence 1216963,
113	13.8	72.6	22	11	US-10-310-914A-296680	Sequence 296680,	c 186	13.4	70.5	19	10	US-10-922-544-94	Sequence 94, Appl
114	13.8	72.6	22	11	US-10-310-914A-296835	Sequence 296835,	c 187	13.4	70.5	19	10	US-10-922-544-268	Sequence 268, Appl
115	13.8	72.6	22	11	US-10-310-914A-296996	Sequence 296996,	c 188	13.4	70.5	19	11	US-10-310-914A-100341	Sequence 100341,
116	13.8	72.6	22	11	US-10-310-914A-297151	Sequence 297151,	c 189	13.4	70.5	19	11	US-10-310-914A-302780	Sequence 302780,
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118	13.8	72.6	22	11	US-10-310-914A-297481	Sequence 297481,	c 191	13.4	70.5	19	11	US-10-310-914A-735858	Sequence 735858,
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120	13.8	72.6	22	11	US-10-310-914A-314857	Sequence 314857,	c 193	13.4	70.5	19	11	US-10-310-914A-1039414	Sequence 1039414,
121	13.8	72.6	22	11	US-10-310-914A-552142	Sequence 552142,	c 194	13.4	70.5	19	11	US-10-310-914A-1066092	Sequence 1066092,
122	13.8	72.6	22	11	US-10-310-914A-682895	Sequence 682895,	c 195	13.4	70.5	19	11	US-10-310-914A-1072631	Sequence 1072631,
c 123	13.8	72.6	22	11	US-10-310-914A-811778	Sequence 811778,	c 196	13.4	70.5	19	11	US-10-310-914A-1216952	Sequence 1216952,
c 124	13.8	72.6	22	11	US-10-310-914A-910800	Sequence 910800,	c 197	13.4	70.5	19	11	US-11-083-784-368501	Sequence 368501,
c 125	13.8	72.6	23	9	US-10-871-302-5	Sequence 5, Appl	c 198	13.4	70.5	19	14	US-11-083-784-1188461	Sequence 1188461,
c 126	13.8	72.6	23	11	US-10-310-914A-310955	Sequence 310955,	c 199	13.4	70.5	19	15	US-11-101-244-368501	Sequence 368501,
c 127	13.8	72.6	23	11	US-10-310-914A-360266	Sequence 360266,	c 200	13.4	70.5	19	15	US-11-101-244-1188461	Sequence 1188461,
c 128	13.8	72.6	23	11	US-10-310-914A-577703	Sequence 577703,	201	13.4	70.5	19	15	US-11-101-244-97281	Sequence 97281, A
c 129	13.8	72.6	23	11	US-10-310-914A-663881	Sequence 663881,	c 202	13.4	70.5	20	11	US-10-310-914A-97281	Sequence 100303,
c 130	13.8	72.6	23	11	US-10-310-914A-705003	Sequence 705003,	c 203	13.4	70.5	20	11	US-10-310-914A-100303	Sequence 307663,
c 131	13.8	72.6	23	11	US-10-310-914A-705010	Sequence 705010,	204	13.4	70.5	20	11	US-10-310-914A-307663	Sequence 307666,
c 132	13.8	72.6	23	11	US-10-310-914A-901219	Sequence 901219,	c 205	13.4	70.5	20	11	US-10-310-914A-307687	Sequence 310954,
c 133	13.8	72.6	23	11	US-10-310-914A-961700	Sequence 961700,	c 206	13.4	70.5	20	11	US-10-310-914A-416998	Sequence 416998,
c 134	13.8	72.6	23	11	US-10-310-914A-1052365	Sequence 1052365,	c 207	13.4	70.5	20	11	US-10-310-914A-455873	Sequence 455873,
c 135	13.8	72.6	24	11	US-10-310-914A-213800	Sequence 213800,	c 208	13.4	70.5	20	11	US-10-310-914A-669347	Sequence 669347,
c 136	13.8	72.6	24	11	US-10-310-914A-213805	Sequence 213805,	c 209	13.4	70.5	20	11	US-10-310-914A-808545	Sequence 808545,
c 137	13.8	72.6	24	11	US-10-310-914A-257978	Sequence 257978,	c 210	13.4	70.5	20	11	US-10-310-914A-808545	Sequence 910802,
c 138	13.8	72.6	24	11	US-10-310-914A-482250	Sequence 482250,	c 211	13.4	70.5	20	11	US-10-310-914A-808545	Sequence 73953, A
c 139	13.8	72.6	24	11	US-10-310-914A-562342	Sequence 562342,	c 212	13.4	70.5	20	11	US-10-310-914A-84238	Sequence 84238, A
c 140	13.8	72.6	24	11	US-10-310-914A-562351	Sequence 562351,	c 213	13.4	70.5	21	11	US-10-310-914A-73953	Sequence 73953, A
c 141	13.8	72.6	24	11	US-10-310-914A-705014	Sequence 705014,	c 214	13.4	70.5	21	11	US-10-310-914A-74063	Sequence 74063, A
c 142	13.8	72.6	24	11	US-10-310-914A-705042	Sequence 705042,	c 215	13.4	70.5	21	11	US-10-310-914A-84238	Sequence 97278, A
c 143	13.8	72.6	24	11	US-10-310-914A-811880	Sequence 811880,	c 216	13.4	70.5	21	11	US-10-310-914A-97278	Sequence 455893,
c 144	13.8	72.6	25	8	US-10-719-956-498100	Sequence 498100,	c 217	13.4	70.5	21	11	US-10-310-914A-455893	Sequence 562350,
c 145	13.8	72.6	25	10	US-10-750-185-7642	Sequence 7642, Ap	c 218	13.4	70.5	21	11	US-10-310-914A-562350	Sequence 663464,
c 146	13.8	72.6	25	10	US-10-750-185-8473	Sequence 8473, Ap	c 219	13.4	70.5	21	11	US-10-310-914A-669353	Sequence 669353,
c 147	13.8	72.6	25	10	US-10-750-623-7642	Sequence 7642, Ap	c 220	13.4	70.5	21	11	US-10-310-914A-669355	Sequence 669355,
c 148	13.8	72.6	25	10	US-10-750-623-8473	Sequence 8473, Ap	c 221	13.4	70.5	21	11	US-10-310-914A-1011823	Sequence 1011823,
c 149	13.8	72.6	25	11	US-10-310-914A-97244	Sequence 97244, A	c 222	13.4	70.5	21	11	US-10-310-914A-1011823	Sequence 73954, A
c 150	13.8	72.6	25	11	US-10-310-914A-213820	Sequence 213820,	c 223	13.4	70.5	22	11	US-10-310-914A-13954	Sequence 166169,
c 151	13.8	72.6	25	11	US-10-310-914A-385338	Sequence 385338,	c 224	13.4	70.5	22	11	US-10-310-914A-166169	Sequence 454990,
c 152	13.8	72.6	25	13	US-11-060-756-134938	Sequence 134938,	c 225	13.4	70.5	22	11	US-10-310-914A-454990	Sequence 454990,
c 153	13.8	72.6	25	13	US-11-060-756-194392	Sequence 194392,	c 226	13.4	70.5	22	11	US-10-310-914A-455793	Sequence 455793,
c 154	13.8	72.6	25	13	US-11-060-756-263781	Sequence 263781,	c 227	13.4	70.5	22	11	US-10-310-914A-455874	Sequence 455874,
c 155	13.8	72.6	25	15	US-11-121-849-468319	Sequence 468319,	c 228	13.4	70.5	22	11	US-10-310-914A-777833	Sequence 777833,
c 156	13.8	72.6	26	11	US-10-310-914A-705043	Sequence 705043,	c 229	13.4	70.5	22	11	US-10-310-914A-1037133	Sequence 1037133,
c 157	13.8	72.6	27	11	US-10-310-914A-294431	Sequence 294431,	c 230	13.4	70.5	23	11	US-10-310-914A-1058183	Sequence 1058183,
c 158	13.8	72.6	27	11	US-10-310-914A-294596	Sequence 294596,	c 231	13.4	70.5	23	11	US-10-310-914A-74064	Sequence 74064, A
c 159	13.8	72.6	27	11	US-10-310-914A-294779	Sequence 294779,	c 232	13.4	70.5	23	11	US-10-310-914A-213803	Sequence 213803,
c 160	13.8	72.6	27	11	US-10-310-914A-294963	Sequence 294963,	c 233	13.4	70.5	23	11	US-10-310-914A-216869	Sequence 216869,
c 161	13.8	72.6	27	11	US-10-310-914A-295292	Sequence 295292,	c 234	13.4	70.5	23	11	US-10-310-914A-216870	Sequence 216870,
c 162	13.8	72.6	27	11	US-10-310-914A-295446	Sequence 295446,	c 235	13.4	70.5	23	11	US-10-310-914A-388921	Sequence 388921,
c 163	13.8	72.6	27	11	US-10-310-914A-295598	Sequence 295598,	c 236	13.4	70.5	23	11	US-10-310-914A-777805	Sequence 777805,

237	13.4	70.5	23	11	US-10-310-914A-777822	Sequence 777822,	310	13.2	69.5	25	10	US-10-956-157-229682	Sequence 229682,
238	13.4	70.5	23	11	US-10-310-914A-1025782	Sequence 1025782,	311	13.2	69.5	25	10	US-10-956-157-229683	Sequence 229683,
239	13.4	70.5	24	11	US-10-310-914A-97243	Sequence 97243, A	312	13.2	69.5	25	10	US-10-956-157-229684	Sequence 229684,
240	13.4	70.5	24	11	US-10-310-914A-735904	Sequence 735904,	313	13.2	69.5	25	11	US-10-310-914A-1316854	Sequence 1316854,
241	13.4	70.5	24	11	US-10-310-914A-959232	Sequence 959232,	314	13.2	69.5	25	11	US-10-310-914A-659406	Sequence 659406,
242	13.4	70.5	25	11	US-10-310-914A-388925	Sequence 388925,	C 315	13.2	69.5	25	11	US-10-310-914A-1154445	Sequence 1154445,
C 243	13.4	70.5	27	11	US-10-310-914A-434377	Sequence 434377,	316	13.2	69.5	25	13	US-11-036-317-178245	Sequence 178245,
C 244	13.2	69.5	18	7	US-10-349-143-9827	Sequence 9827, Ap	317	13.2	69.5	25	13	US-11-036-317-183808	Sequence 183808,
C 245	13.2	69.5	18	11	US-10-310-914A-115803	Sequence 115803,	318	13.2	69.5	25	13	US-11-036-317-247130	Sequence 247130,
C 246	13.2	69.5	18	11	US-10-310-914A-442574	Sequence 442574,	319	13.2	69.5	25	13	US-11-036-317-256038	Sequence 256038,
C 247	13.2	69.5	18	11	US-10-310-914A-767354	Sequence 767354,	320	13.2	69.5	25	13	US-11-036-317-256144	Sequence 256144,
C 248	13.2	69.5	18	11	US-10-310-914A-969834	Sequence 969834,	321	13.2	69.5	25	13	US-11-036-317-291683	Sequence 291683,
C 249	13.2	69.5	18	11	US-10-310-914A-1039492	Sequence 1039492,	322	13.2	69.5	25	13	US-11-036-317-292484	Sequence 292484,
C 250	13.2	69.5	18	11	US-10-310-914A-1039493	Sequence 1039493,	323	13.2	69.5	25	13	US-11-036-317-311345	Sequence 311345,
C 251	13.2	69.5	18	11	US-10-310-914A-1207995	Sequence 1207995,	324	13.2	69.5	25	13	US-11-036-317-327757	Sequence 327757,
C 252	13.2	69.5	19	11	US-10-310-914A-195423	Sequence 195423,	325	13.2	69.5	25	13	US-11-036-317-864691	Sequence 864691,
C 253	13.2	69.5	19	11	US-10-310-914A-290076	Sequence 290076,	326	13.2	69.5	25	13	US-11-036-317-908932	Sequence 908932,
C 254	13.2	69.5	19	11	US-10-310-914A-841604	Sequence 841604,	327	13.2	69.5	25	13	US-11-036-317-929668	Sequence 929668,
C 255	13.2	69.5	19	11	US-10-310-914A-917073	Sequence 917073,	C 328	13.2	69.5	25	13	US-11-036-317-930935	Sequence 930935,
C 256	13.2	69.5	19	14	US-11-083-784-790058	Sequence 790058,	C 329	13.2	69.5	25	13	US-11-036-317-980151	Sequence 980151,
C 257	13.2	69.5	19	14	US-11-083-784-1577418	Sequence 1577418,	C 330	13.2	69.5	25	15	US-11-121-849-29929	Sequence 29929, A
C 258	13.2	69.5	19	15	US-11-101-244-790058	Sequence 790058,	C 331	13.2	69.5	25	15	US-11-121-849-91257	Sequence 91257, A
C 259	13.2	69.5	19	15	US-11-101-244-1577418	Sequence 1577418,	C 332	13.2	69.5	25	16	US-11-136-527-222834	Sequence 222834,
C 260	13.2	69.5	20	7	US-10-352-179-24	Sequence 24, Appl	C 333	13.2	69.5	25	16	US-11-136-527-222839	Sequence 222839,
C 261	13.2	69.5	20	11	US-10-310-914A-261339	Sequence 261339,	C 334	13.2	69.5	26	11	US-10-310-914A-1154412	Sequence 1154412,
C 262	13.2	69.5	20	11	US-10-310-914A-649974	Sequence 649974,	C 335	13.2	69.5	28	11	US-10-310-914A-824016	Sequence 824016,
C 263	13.2	69.5	20	11	US-10-310-914A-717339	Sequence 717339,	C 336	13.2	69.5	28	11	US-10-310-914A-824017	Sequence 824017,
C 264	13.2	69.5	20	11	US-10-310-914A-720599	Sequence 720599,	C 337	13.2	69.5	30	11	US-10-310-914A-1154446	Sequence 1154446,
C 265	13.2	69.5	20	11	US-10-310-914A-905817	Sequence 905817,	C 338	13	68.4	13	9	US-10-257-017B-221109	Sequence 221109, A
C 266	13.2	69.5	20	11	US-10-310-914A-1093322	Sequence 1093322,	C 339	13	68.4	13	9	US-10-257-017B-221110	Sequence 221110, A
C 267	13.2	69.5	20	11	US-10-310-914A-1181248	Sequence 1181248,	C 340	13	68.4	18	11	US-10-310-914A-173366	Sequence 173366,
C 268	13.2	69.5	20	11	US-10-310-914A-1351173	Sequence 1351173,	C 341	13	68.4	18	11	US-10-310-914A-343564	Sequence 343564,
C 269	13.2	69.5	21	3	US-09-792-686A-21	Sequence 21, Appl	C 342	13	68.4	18	11	US-10-310-914A-343565	Sequence 343565,
C 270	13.2	69.5	21	11	US-10-310-914A-195613	Sequence 195613,	C 343	13	68.4	18	11	US-10-310-914A-613668	Sequence 613668,
C 271	13.2	69.5	21	11	US-10-310-914A-281171	Sequence 281171,	C 344	13	68.4	19	11	US-10-310-914A-661032	Sequence 661032,
C 272	13.2	69.5	21	11	US-10-310-914A-326296	Sequence 326296,	C 345	13	68.4	19	11	US-10-310-914A-303294	Sequence 303294,
C 273	13.2	69.5	21	11	US-10-310-914A-483084	Sequence 483084,	C 346	13	68.4	20	11	US-10-310-914A-100501	Sequence 100501,
C 274	13.2	69.5	21	11	US-10-310-914A-651050	Sequence 651050,	C 347	13	68.4	20	11	US-10-310-914A-252950	Sequence 252950,
C 275	13.2	69.5	21	11	US-10-310-914A-761684	Sequence 761684,	C 348	13	68.4	20	11	US-10-310-914A-1277951	Sequence 1277951,
C 276	13.2	69.5	21	11	US-10-310-914A-841608	Sequence 841608,	C 349	13	68.4	21	11	US-10-310-914A-406657	Sequence 406657,
C 277	13.2	69.5	21	11	US-10-310-914A-916746	Sequence 916746,	C 350	13	68.4	21	11	US-10-310-914A-695331	Sequence 695331,
C 278	13.2	69.5	21	11	US-10-310-914A-932978	Sequence 932978,	C 351	13	68.4	22	11	US-10-310-914A-148933	Sequence 148933,
C 279	13.2	69.5	21	11	US-10-310-914A-1126558	Sequence 1126558,	C 352	13	68.4	22	11	US-10-310-914A-252920	Sequence 252920,
C 280	13.2	69.5	21	11	US-10-310-914A-127657	Sequence 127657,	C 353	13	68.4	22	11	US-10-310-914A-1065861	Sequence 1065861,
C 281	13.2	69.5	22	11	US-10-310-914A-140374	Sequence 140374,	C 354	13	68.4	23	11	US-10-310-914A-613717	Sequence 613717,
C 282	13.2	69.5	22	11	US-10-310-914A-326329	Sequence 326329,	C 355	13	68.4	24	11	US-10-310-914A-173334	Sequence 173334,
C 283	13.2	69.5	22	11	US-10-310-914A-463641	Sequence 463641,	C 356	13	68.4	25	10	US-10-956-157-207666	Sequence 207666,
C 284	13.2	69.5	22	11	US-10-310-914A-690897	Sequence 690897,	C 357	13	68.4	25	10	US-10-956-157-207667	Sequence 207667,
C 285	13.2	69.5	22	11	US-10-310-914A-715072	Sequence 715072,	C 358	13	68.4	25	11	US-10-310-914A-871513	Sequence 871513,
C 286	13.2	69.5	22	11	US-10-310-914A-823986	Sequence 823986,	C 359	13	68.4	27	11	US-10-310-914A-252918	Sequence 252918,
C 287	13.2	69.5	22	11	US-10-310-914A-1351129	Sequence 1351129,	C 360	12.8	67.4	18	11	US-10-310-914A-257971	Sequence 257971,
C 288	13.2	69.5	23	11	US-10-310-914A-192733	Sequence 192733,	C 361	12.8	67.4	18	11	US-10-310-914A-335332	Sequence 335332,
C 289	13.2	69.5	23	11	US-10-310-914A-317803	Sequence 317803,	C 362	12.8	67.4	18	11	US-10-310-914A-369326	Sequence 369326,
C 290	13.2	69.5	23	11	US-10-310-914A-334910	Sequence 334910,	C 363	12.8	67.4	18	11	US-10-310-914A-873278	Sequence 873278,
C 291	13.2	69.5	23	11	US-10-310-914A-463679	Sequence 463679,	C 364	12.8	67.4	18	11	US-10-310-914A-1272786	Sequence 1272786,
C 292	13.2	69.5	23	11	US-10-310-914A-500461	Sequence 500461,	C 365	12.8	67.4	18	11	US-10-310-914A-1378375	Sequence 1378375,
C 293	13.2	69.5	23	11	US-10-310-914A-619988	Sequence 619988,	C 366	12.8	67.4	19	11	US-10-310-914A-51132	Sequence 51132, A
C 294	13.2	69.5	23	11	US-10-310-914A-651051	Sequence 651051,	C 367	12.8	67.4	19	11	US-10-310-914A-95820	Sequence 95820, A
C 295	13.2	69.5	23	11	US-10-310-914A-824229	Sequence 824229,	C 368	12.8	67.4	19	11	US-10-310-914A-172772	Sequence 172772,
C 296	13.2	69.5	23	11	US-10-310-914A-904077	Sequence 904077,	C 369	12.8	67.4	19	11	US-10-310-914A-257972	Sequence 257972,
C 297	13.2	69.5	23	11	US-10-310-914A-976914	Sequence 976914,	C 370	12.8	67.4	19	11	US-10-310-914A-474111	Sequence 474111,
C 298	13.2	69.5	24	11	US-10-310-914A-1154444	Sequence 1154444,	C 371	12.8	67.4	19	11	US-10-310-914A-500548	Sequence 500548,
C 299	13.2	69.5	24	11	US-10-310-914A-115836	Sequence 115836,	C 372	12.8	67.4	19	11	US-10-310-914A-577702	Sequence 577702,
C 300	13.2	69.5	24	11	US-10-310-914A-194642	Sequence 194642,	C 373	12.8	67.4	19	11	US-10-310-914A-716025	Sequence 716025,
C 301	13.2	69.5	24	11	US-10-310-914A-326330	Sequence 326330,	C 374	12.8	67.4	19	11	US-10-310-914A-847855	Sequence 847855,
C 302	13.2	69.5	24	11	US-10-310-914A-619989	Sequence 619989,	C 375	12.8	67.4	19	11	US-10-310-914A-1093299	Sequence 1093299,
C 303	13.2	69.5	24	11	US-10-310-914A-735164	Sequence 735164,	C 376	12.8	67.4	19	11	US-10-310-914A-1142682	Sequence 1142682,
C 304	13.2	69.5	24	11	US-10-310-914A-916747	Sequence 916747,	C 377	12.8	67.4	19	11	US-10-310-914A-1378387	Sequence 1378387,
C 305	13.2	69.5	24	11	US-10-310-914A-1103589	Sequence 1103589,	C 378	12.8	67.4	19	14	US-11-083-784-486457	Sequence 486457,
C 306	13.2	69.5	24	11	US-10-310-914A-1181254	Sequence 1181254,	C 379	12.8	67.4	19	14	US-11-083-784-487336	Sequence 487336,
C 307	13.2	69.5	24	11	US-10-310-914A-1351138	Sequence 1351138,	C 380	12.8	67.4	19	14	US-11-083-784-487412	Sequence 487412,
C 308	13.2	69.5	24	11	US-10-310-914A-1361528	Sequence 1361528,	C 381	12.8	67.4	19	14	US-11-083-784-715680	Sequence 715680,
C 309	13.2	69.5	25	9	US-10-719-900-595274	Sequence 595274,	C 382	12.8	67.4	19	14	US-11-083-784-1513349	Sequence 1513349,

383	12.8	67.4	19	14	US-11-083-784-1563591	Sequence 1563591,	456	12.8	67.4	25	11	US-10-310-914A-404846	Sequence 404846,
C 384	12.8	67.4	19	15	US-11-101-244-486457	Sequence 486457,	457	12.8	67.4	25	13	US-11-036-317-616459	Sequence 616459,
C 385	12.8	67.4	19	15	US-11-101-244-487336	Sequence 487336,	c 458	12.8	67.4	25	13	US-11-036-317-655548	Sequence 655548,
C 386	12.8	67.4	19	15	US-11-101-244-487412	Sequence 487412,	c 459	12.8	67.4	25	13	US-11-060-756-134993	Sequence 134993,
C 387	12.8	67.4	19	15	US-11-101-244-487412	Sequence 487412,	c 460	12.8	67.4	25	13	US-11-060-756-170180	Sequence 170180,
C 388	12.8	67.4	19	15	US-11-101-244-487412	Sequence 487412,	c 461	12.8	67.4	25	13	US-11-060-756-170181	Sequence 170181,
C 389	12.8	67.4	19	15	US-11-101-244-487412	Sequence 487412,	c 462	12.8	67.4	25	13	US-11-060-756-183698	Sequence 183698,
C 390	12.8	67.4	19	15	US-11-101-244-487412	Sequence 487412,	c 463	12.8	67.4	25	13	US-11-060-756-212339	Sequence 212339,
C 391	12.8	67.4	20	7	US-09-922-549B-42	Sequence 42, Appl	c 464	12.8	67.4	25	13	US-11-060-756-213328	Sequence 213328,
C 392	12.8	67.4	20	11	US-10-114-739A-42	Sequence 42, Appl	c 465	12.8	67.4	25	13	US-11-060-756-255120	Sequence 255120,
C 393	12.8	67.4	20	11	US-10-310-914A-335395	Sequence 335395,	c 466	12.8	67.4	25	13	US-11-060-756-255121	Sequence 255121,
C 394	12.8	67.4	20	11	US-10-310-914A-338100	Sequence 338100,	c 467	12.8	67.4	25	15	US-11-121-849-15773	Sequence 15773, A
C 395	12.8	67.4	20	11	US-10-310-914A-605671	Sequence 605671,	c 468	12.8	67.4	25	15	US-11-121-849-44677	Sequence 44677, A
C 396	12.8	67.4	20	11	US-10-310-914A-624814	Sequence 624814,	c 469	12.8	67.4	25	15	US-11-121-849-337689	Sequence 337689,
C 397	12.8	67.4	20	11	US-10-310-914A-624820	Sequence 624820,	c 470	12.8	67.4	25	15	US-11-121-849-456615	Sequence 456615,
C 398	12.8	67.4	20	11	US-10-310-914A-762570	Sequence 762570,	c 471	12.8	67.4	25	16	US-11-136-527-190983	Sequence 190983,
C 399	12.8	67.4	20	11	US-10-310-914A-961930	Sequence 961930,	c 472	12.8	67.4	25	16	US-11-136-527-190985	Sequence 190985,
C 400	12.8	67.4	20	11	US-10-310-914A-1211365	Sequence 1211365,	c 473	12.8	67.4	26	10	US-10-708-204-5624	Sequence 5624, Ap
C 401	12.8	67.4	20	11	US-10-310-914A-1344669	Sequence 1344669,	c 474	12.8	67.4	27	11	US-10-310-914A-1039035	Sequence 1039035,
C 402	12.8	67.4	21	11	US-10-310-914A-333343	Sequence 333343,	c 475	12.8	67.4	29	11	US-10-310-914A-467540	Sequence 467540,
C 403	12.8	67.4	21	11	US-10-310-914A-624816	Sequence 624816,	c 476	12.8	67.4	30	9	US-10-615-343-5	Sequence 5, Appl
C 404	12.8	67.4	21	11	US-10-310-914A-682894	Sequence 682894,	c 477	12.8	66.3	19	10	US-10-923-640-16	Sequence 16, Appl
C 405	12.8	67.4	21	11	US-10-310-914A-816882	Sequence 816882,	c 478	12.6	66.3	19	10	US-10-923-640-72	Sequence 72, Appl
C 406	12.8	67.4	21	11	US-10-310-914A-901200	Sequence 901200,	c 479	12.6	66.3	19	10	US-10-923-330-88	Sequence 88, Appl
C 407	12.8	67.4	21	11	US-10-310-914A-1063512	Sequence 1063512,	c 480	12.6	66.3	19	10	US-10-923-330-311	Sequence 311, App
C 408	12.8	67.4	22	11	US-10-708-204-5604	Sequence 5604, Ap	c 481	12.6	66.3	19	11	US-10-310-914A-65168	Sequence 65168, A
C 409	12.8	67.4	22	11	US-10-310-914A-95799	Sequence 95799, A	c 482	12.6	66.3	19	11	US-10-310-914A-72981	Sequence 72981, A
C 410	12.8	67.4	22	11	US-10-310-914A-142870	Sequence 142870,	c 483	12.6	66.3	19	11	US-10-310-914A-157287	Sequence 157287,
C 411	12.8	67.4	22	11	US-10-310-914A-368975	Sequence 368975,	c 484	12.6	66.3	19	11	US-10-310-914A-176902	Sequence 176902,
C 412	12.8	67.4	22	11	US-10-310-914A-369359	Sequence 369359,	c 485	12.6	66.3	19	11	US-10-310-914A-203711	Sequence 203711,
C 413	12.8	67.4	22	11	US-10-310-914A-474064	Sequence 474064,	c 486	12.6	66.3	19	11	US-10-310-914A-203712	Sequence 203712,
C 414	12.8	67.4	22	11	US-10-310-914A-624815	Sequence 624815,	c 487	12.6	66.3	19	11	US-10-310-914A-222505	Sequence 222505,
C 415	12.8	67.4	22	11	US-10-310-914A-624964	Sequence 624964,	c 488	12.6	66.3	19	11	US-10-310-914A-232048	Sequence 232048,
C 416	12.8	67.4	22	11	US-10-310-914A-663876	Sequence 663876,	c 489	12.6	66.3	19	11	US-10-310-914A-232049	Sequence 232049,
C 417	12.8	67.4	22	11	US-10-310-914A-738941	Sequence 738941,	c 490	12.6	66.3	19	11	US-10-310-914A-322557	Sequence 322557,
C 418	12.8	67.4	22	11	US-10-310-914A-922788	Sequence 922788,	c 491	12.6	66.3	19	11	US-10-310-914A-390844	Sequence 390844,
C 419	12.8	67.4	22	11	US-10-310-914A-966864	Sequence 966864,	c 492	12.6	66.3	19	11	US-10-310-914A-508541	Sequence 508541,
C 420	12.8	67.4	22	11	US-10-310-914A-1039045	Sequence 1039045,	c 493	12.6	66.3	19	11	US-10-310-914A-519305	Sequence 519305,
C 421	12.8	67.4	22	11	US-10-310-914A-1063490	Sequence 1063490,	c 494	12.6	66.3	19	11	US-10-310-914A-719506	Sequence 719506,
C 422	12.8	67.4	22	11	US-10-310-914A-1157328	Sequence 1157328,	c 495	12.6	66.3	19	11	US-10-310-914A-746346	Sequence 746346,
C 423	12.8	67.4	22	11	US-10-310-914A-1272787	Sequence 1272787,	c 496	12.6	66.3	19	11	US-10-310-914A-746853	Sequence 746853,
C 424	12.8	67.4	22	11	US-10-310-914A-1339872	Sequence 1339872,	c 497	12.6	66.3	19	11	US-10-310-914A-766602	Sequence 766602,
C 425	12.8	67.4	22	11	US-10-310-914A-1344662	Sequence 1344662,	c 498	12.6	66.3	19	11	US-10-310-914A-899946	Sequence 899946,
C 426	12.8	67.4	23	11	US-10-310-914A-194840	Sequence 194840,	c 499	12.6	66.3	19	11	US-10-310-914A-956881	Sequence 956881,
C 427	12.8	67.4	23	11	US-10-310-914A-194847	Sequence 194847,	c 500	12.6	66.3	19	11	US-10-310-914A-1019621	Sequence 1019621,
C 428	12.8	67.4	23	11	US-10-310-914A-257983	Sequence 257983,	c 501	12.6	66.3	19	11	US-10-310-914A-1047575	Sequence 1047575,
C 429	12.8	67.4	23	11	US-10-310-914A-381034	Sequence 381034,	c 502	12.6	66.3	19	11	US-10-310-914A-1117694	Sequence 1117694,
C 430	12.8	67.4	23	11	US-10-310-914A-381038	Sequence 381038,	c 503	12.6	66.3	19	11	US-10-310-914A-1126936	Sequence 1126936,
C 431	12.8	67.4	23	11	US-10-310-914A-562349	Sequence 562349,	c 504	12.6	66.3	19	11	US-10-310-914A-1258054	Sequence 1258054,
C 432	12.8	67.4	23	11	US-10-310-914A-762701	Sequence 762701,	c 505	12.6	66.3	19	14	US-11-083-784-276730	Sequence 276730,
C 433	12.8	67.4	23	11	US-10-310-914A-847833	Sequence 847833,	c 506	12.6	66.3	19	14	US-11-083-784-276730	Sequence 276730,
C 434	12.8	67.4	23	11	US-10-310-914A-847834	Sequence 847834,	c 507	12.6	66.3	19	14	US-11-083-784-276823	Sequence 276823,
C 435	12.8	67.4	23	11	US-10-310-914A-952477	Sequence 952477,	c 508	12.6	66.3	19	14	US-11-083-784-1453943	Sequence 1453943,
C 436	12.8	67.4	24	11	US-10-310-914A-1020923	Sequence 1020923,	c 509	12.6	66.3	19	14	US-11-083-784-1572356	Sequence 1572356,
C 437	12.8	67.4	24	11	US-10-310-914A-142852	Sequence 142852,	c 510	12.6	66.3	19	15	US-11-101-244-276636	Sequence 276636,
C 438	12.8	67.4	24	11	US-10-310-914A-172765	Sequence 172765,	c 511	12.6	66.3	19	15	US-11-101-244-276730	Sequence 276730,
C 439	12.8	67.4	24	11	US-10-310-914A-188749	Sequence 188749,	c 512	12.6	66.3	19	15	US-11-101-244-276823	Sequence 276823,
C 440	12.8	67.4	24	11	US-10-310-914A-354348	Sequence 354348,	c 513	12.6	66.3	19	15	US-11-101-244-1453943	Sequence 1453943,
C 441	12.8	67.4	24	11	US-10-310-914A-655918	Sequence 655918,	c 514	12.6	66.3	19	15	US-11-101-244-1572356	Sequence 1572356,
C 442	12.8	67.4	24	11	US-10-310-914A-703227	Sequence 703227,	c 515	12.6	66.3	20	11	US-10-310-914A-103725	Sequence 103725,
C 443	12.8	67.4	24	11	US-10-310-914A-703227	Sequence 703227,	c 516	12.6	66.3	20	11	US-10-310-914A-321532	Sequence 321532,
C 444	12.8	67.4	24	11	US-10-310-914A-1260686	Sequence 1260686,	c 517	12.6	66.3	20	11	US-10-310-914A-510631	Sequence 510631,
C 445	12.8	67.4	25	8	US-10-719-956-222176	Sequence 222176,	c 518	12.6	66.3	20	11	US-10-310-914A-510632	Sequence 510632,
C 446	12.8	67.4	25	9	US-10-719-900-138454	Sequence 138454,	c 519	12.6	66.3	20	11	US-10-310-914A-719554	Sequence 719554,
C 447	12.8	67.4	25	9	US-10-719-900-629679	Sequence 629679,	c 520	12.6	66.3	20	11	US-10-310-914A-1084091	Sequence 1084091,
C 448	12.8	67.4	25	9	US-10-719-900-750276	Sequence 750276,	c 521	12.6	66.3	20	11	US-10-310-914A-1084317	Sequence 1084317,
C 449	12.8	67.4	25	9	US-10-719-900-759595	Sequence 759595,	c 522	12.6	66.3	20	11	US-10-310-914A-1216178	Sequence 1216178,
C 450	12.8	67.4	25	9	US-10-719-900-858803	Sequence 858803,	c 523	12.6	66.3	20	11	US-10-310-914A-1216477	Sequence 1216477,
C 451	12.8	67.4	25	10	US-10-956-157-89169	Sequence 89169, A	c 524	12.6	66.3	21	9	US-10-751-736-539	Sequence 539, App
C 452	12.8	67.4	25	10	US-10-956-157-89169	Sequence 89169, A	c 525	12.6	66.3	21	10	US-10-770-726-26016	Sequence 26016, A
C 453	12.8	67.4	25	11	US-10-310-914A-95813	Sequence 95813, A	c 526	12.6	66.3	21	11	US-10-310-914A-73613	Sequence 73613, A
C 454	12.8	67.4	25	11	US-10-310-914A-339081	Sequence 339081,	c 527	12.6	66.3	21	11	US-10-310-914A-73614	Sequence 73614, A
C 455	12.8	67.4	25	11	US-10-310-914A-354339	Sequence 354339,	c 528	12.6	66.3	21	11	US-10-310-914A-73615	Sequence 73615, A

529	12.6	66.3	21	11	US-10-310-914A-94381	Sequence 94381, A	602	12.6	66.3	24	11	US-10-310-914A-94360	Sequence 94260, A
530	12.6	66.3	21	11	US-10-310-914A-103727	Sequence 103727,	603	12.6	66.3	24	11	US-10-310-914A-147960	Sequence 147960,
531	12.6	66.3	21	11	US-10-310-914A-222506	Sequence 222506,	604	12.6	66.3	24	11	US-10-310-914A-227909	Sequence 227909,
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533	12.6	66.3	21	11	US-10-310-914A-325161	Sequence 325161,	c 606	12.6	66.3	24	11	US-10-310-914A-390831	Sequence 390831,
534	12.6	66.3	21	11	US-10-310-914A-643562	Sequence 643562,	c 607	12.6	66.3	24	11	US-10-310-914A-413470	Sequence 413470,
535	12.6	66.3	21	11	US-10-310-914A-683746	Sequence 683746,	c 608	12.6	66.3	24	11	US-10-310-914A-535808	Sequence 535808,
536	12.6	66.3	21	11	US-10-310-914A-700705	Sequence 700705,	c 609	12.6	66.3	24	11	US-10-310-914A-535930	Sequence 535930,
537	12.6	66.3	21	11	US-10-310-914A-700719	Sequence 700719,	c 610	12.6	66.3	24	11	US-10-310-914A-605839	Sequence 605839,
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541	12.6	66.3	21	11	US-10-310-914A-936911	Sequence 936911,	c 614	12.6	66.3	24	11	US-10-310-914A-1084350	Sequence 1084350,
542	12.6	66.3	21	11	US-10-310-914A-955342	Sequence 955342,	c 615	12.6	66.3	24	11	US-10-310-914A-1118720	Sequence 1118720,
543	12.6	66.3	21	11	US-10-310-914A-993013	Sequence 993013,	c 616	12.6	66.3	24	11	US-10-310-914A-1166895	Sequence 1166895,
544	12.6	66.3	21	11	US-10-310-914A-1006899	Sequence 1006899,	c 617	12.6	66.3	24	11	US-10-310-914A-1216210	Sequence 1216210,
545	12.6	66.3	21	11	US-10-310-914A-1162708	Sequence 1162708,	c 618	12.6	66.3	24	11	US-10-310-914A-1377536	Sequence 1377536,
546	12.6	66.3	21	11	US-10-310-914A-1242817	Sequence 1242817,	c 619	12.6	66.3	25	3	US-09-766-399-38	Sequence 38, Appl
547	12.6	66.3	22	10	US-10-708-204-124	Sequence 124, App	c 620	12.6	66.3	25	8	US-10-603-642-38	Sequence 373, Appl
548	12.6	66.3	22	10	US-10-708-204-659	Sequence 659, App	c 621	12.6	66.3	25	9	US-10-719-900-373	Sequence 917855,
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551	12.6	66.3	22	10	US-10-708-204-1846	Sequence 1846, App	c 624	12.6	66.3	25	10	US-10-956-157-190725	Sequence 190725,
552	12.6	66.3	22	10	US-10-708-204-1928	Sequence 1928, App	c 625	12.6	66.3	25	10	US-10-956-157-208395	Sequence 208395,
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554	12.6	66.3	22	10	US-10-708-204-2360	Sequence 2360, App	c 627	12.6	66.3	25	10	US-10-956-157-229486	Sequence 229486,
555	12.6	66.3	22	10	US-10-708-204-2452	Sequence 2452, App	c 628	12.6	66.3	25	10	US-10-956-157-267537	Sequence 267537,
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558	12.6	66.3	22	11	US-10-310-914A-73635	Sequence 73635, A	c 631	12.6	66.3	25	10	US-10-956-157-275961	Sequence 275961,
559	12.6	66.3	22	11	US-10-310-914A-102602	Sequence 102602,	c 632	12.6	66.3	25	11	US-10-310-914A-75915	Sequence 75915, A
560	12.6	66.3	22	11	US-10-310-914A-153905	Sequence 153905,	c 633	12.6	66.3	25	11	US-10-310-914A-1084144	Sequence 1084144,
561	12.6	66.3	22	11	US-10-310-914A-212945	Sequence 212945,	c 634	12.6	66.3	25	11	US-10-310-914A-1108583	Sequence 1108583,
562	12.6	66.3	22	11	US-10-310-914A-212945	Sequence 212945,	c 635	12.6	66.3	25	11	US-10-310-914A-1216533	Sequence 1216533,
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567	12.6	66.3	22	11	US-10-310-914A-356416	Sequence 356416,	c 640	12.6	66.3	25	13	US-11-036-317-312547	Sequence 312547,
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571	12.6	66.3	22	11	US-10-310-914A-825664	Sequence 825664,	c 644	12.6	66.3	25	13	US-11-036-317-335845	Sequence 335845,
572	12.6	66.3	22	11	US-10-310-914A-1084143	Sequence 1084143,	c 645	12.6	66.3	25	13	US-11-036-317-344957	Sequence 344957,
573	12.6	66.3	22	11	US-10-310-914A-1084371	Sequence 1084371,	c 646	12.6	66.3	25	13	US-11-036-317-356885	Sequence 356885,
574	12.6	66.3	22	11	US-10-310-914A-1126718	Sequence 1126718,	c 647	12.6	66.3	25	13	US-11-036-317-362794	Sequence 362794,
575	12.6	66.3	22	11	US-10-310-914A-1215197	Sequence 1215197,	c 648	12.6	66.3	25	13	US-11-036-317-383645	Sequence 383645,
576	12.6	66.3	22	11	US-10-310-914A-1216233	Sequence 1216233,	c 649	12.6	66.3	25	13	US-11-036-317-389870	Sequence 389870,
577	12.6	66.3	22	11	US-10-310-914A-1216532	Sequence 1216532,	c 650	12.6	66.3	25	13	US-11-036-317-391375	Sequence 391375,
578	12.6	66.3	23	11	US-10-310-914A-89521	Sequence 89521, A	c 651	12.6	66.3	25	13	US-11-036-317-397284	Sequence 397284,
579	12.6	66.3	23	11	US-10-310-914A-102570	Sequence 102570,	c 652	12.6	66.3	25	13	US-11-036-317-608023	Sequence 608023,
580	12.6	66.3	23	11	US-10-310-914A-122174	Sequence 122174,	c 653	12.6	66.3	25	13	US-11-036-317-734541	Sequence 734541,
581	12.6	66.3	23	11	US-10-310-914A-153911	Sequence 153911,	c 654	12.6	66.3	25	13	US-11-036-317-865988	Sequence 865988,
582	12.6	66.3	23	11	US-10-310-914A-227940	Sequence 227940,	c 655	12.6	66.3	25	13	US-11-036-317-869589	Sequence 869589,
583	12.6	66.3	23	11	US-10-310-914A-227942	Sequence 227942,	c 656	12.6	66.3	25	13	US-11-036-317-952228	Sequence 952228,
584	12.6	66.3	23	11	US-10-310-914A-267065	Sequence 267065,	c 657	12.6	66.3	25	13	US-11-060-756-183164	Sequence 183164,
585	12.6	66.3	23	11	US-10-310-914A-346254	Sequence 346254,	c 658	12.6	66.3	25	13	US-11-060-756-188596	Sequence 188596,
586	12.6	66.3	23	11	US-10-310-914A-374923	Sequence 374923,	c 659	12.6	66.3	25	13	US-11-060-756-202479	Sequence 202479,
587	12.6	66.3	23	11	US-10-310-914A-410853	Sequence 410853,	c 660	12.6	66.3	25	13	US-11-060-756-262334	Sequence 262334,
588	12.6	66.3	23	11	US-10-310-914A-412726	Sequence 412726,	c 661	12.6	66.3	25	13	US-11-060-756-264459	Sequence 264459,
589	12.6	66.3	23	11	US-10-310-914A-413436	Sequence 413436,	c 662	12.6	66.3	25	13	US-11-121-849-44498	Sequence 44498, A
590	12.6	66.3	23	11	US-10-310-914A-417749	Sequence 417749,	c 663	12.6	66.3	25	15	US-11-121-849-82053	Sequence 82053, A
591	12.6	66.3	23	11	US-10-310-914A-610381	Sequence 610381,	c 664	12.6	66.3	25	15	US-11-121-849-320323	Sequence 320323,
592	12.6	66.3	23	11	US-10-310-914A-610409	Sequence 610409,	c 665	12.6	66.3	25	15	US-11-121-849-323414	Sequence 323414,
593	12.6	66.3	23	11	US-10-310-914A-700706	Sequence 700706,	c 666	12.6	66.3	25	11	US-10-310-914A-356402	Sequence 356402,
594	12.6	66.3	23	11	US-10-310-914A-711840	Sequence 711840,	c 667	12.6	66.3	26	11	US-10-310-914A-676726	Sequence 676726,
595	12.6	66.3	23	11	US-10-310-914A-825681	Sequence 825681,	c 668	12.6	66.3	27	10	US-10-708-204-4762	Sequence 4762, App
596	12.6	66.3	23	11	US-10-310-914A-829170	Sequence 829170,	c 669	12.6	66.3	27	11	US-10-310-914A-1242802	Sequence 1242802,
597	12.6	66.3	23	11	US-10-310-914A-1135643	Sequence 1135643,	c 670	12.6	66.3	27	11	US-10-310-914A-1258454	Sequence 1258454,
598	12.6	66.3	23	11	US-10-310-914A-1162688	Sequence 1162688,	c 671	12.6	66.3	28	11	US-10-310-914A-89656	Sequence 89656, A
599	12.6	66.3	24	3	US-09-951-502A-14	Sequence 14, Appl	c 672	12.6	66.3	28	11	US-10-310-914A-302047	Sequence 302047,
600	12.6	66.3	24	11	US-10-310-914A-73616	Sequence 73616, A	c 673	12.6	66.3	28	11	US-10-310-914A-700720	Sequence 700720,
601	12.6	66.3	24	11	US-10-310-914A-74642	Sequence 74642, A	c 674	12.6	66.3	30	11	US-10-310-914A-212257	Sequence 212257,


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c 967 12.2 64.2 19 11 US-10-310-914A-535859
c 968 12.2 64.2 19 11 US-10-310-914A-550076
c 969 12.2 64.2 19 11 US-10-310-914A-643942
c 970 12.2 64.2 19 11 US-10-310-914A-632531
c 971 12.2 64.2 19 11 US-10-310-914A-735139
c 972 12.2 64.2 19 11 US-10-310-914A-735140
c 973 12.2 64.2 19 11 US-10-310-914A-735140
c 974 12.2 64.2 19 11 US-10-310-914A-741358
c 975 12.2 64.2 19 11 US-10-310-914A-765387
c 976 12.2 64.2 19 11 US-10-310-914A-774771
c 977 12.2 64.2 19 11 US-10-310-914A-833761
c 978 12.2 64.2 19 11 US-10-310-914A-854200
c 979 12.2 64.2 19 11 US-10-310-914A-876219
c 980 12.2 64.2 19 11 US-10-310-914A-880636
c 981 12.2 64.2 19 11 US-10-310-914A-880705
c 982 12.2 64.2 19 11 US-10-310-914A-916252
c 983 12.2 64.2 19 11 US-10-310-914A-922088
c 984 12.2 64.2 19 11 US-10-310-914A-939711
c 985 12.2 64.2 19 11 US-10-310-914A-991974
c 986 12.2 64.2 19 11 US-10-310-914A-1069554
c 987 12.2 64.2 19 11 US-10-310-914A-1078919
c 988 12.2 64.2 19 11 US-10-310-914A-1099644
c 989 12.2 64.2 19 11 US-10-310-914A-1126557
c 990 12.2 64.2 19 11 US-10-310-914A-1139647
c 991 12.2 64.2 19 11 US-10-310-914A-1178997
c 992 12.2 64.2 19 11 US-10-310-914A-1211302
c 993 12.2 64.2 19 11 US-10-310-914A-1306779
c 994 12.2 64.2 19 11 US-10-310-914A-1306852
c 995 12.2 64.2 19 11 US-10-310-914A-1370003
c 996 12.2 64.2 19 11 US-10-310-914A-1381444
c 997 12.2 64.2 19 14 US-11-083-784-9345
c 998 12.2 64.2 19 14 US-11-083-784-88104
c 999 12.2 64.2 19 14 US-11-083-784-116412
c1000 12.2 64.2 19 14 US-11-083-784-128169
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ALIGNMENTS

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RESULT 1
US-10-310-914A-35144
; Sequence 35144, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35144
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-35144
Query Match 100.0%; Score 19; DB 11; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTGCT 19
|||
Db 1 GGAGAAGGGGGTGGGTGCT 19
|||

RESULT 2
US-10-310-914A-1065850/c
; Sequence 1065850, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065850
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065850
Query Match 100.0%; Score 19; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTGCT 19
|||
Db 19 GGAGAAGGGGGTGGGTGCT 1
|||

RESULT 3
US-10-310-914A-148934/c
; Sequence 148934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148934
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148934
Query Match 100.0%; Score 19; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGGTGGGTGCT 19
|||
Db 20 GGAGAAGGGGGTGGGTGCT 2
|||

RESULT 4
US-10-310-914A-148966/c
; Sequence 148966, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148966
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148966
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Query Match 94.7%; Score 18; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGC 18
|||||
Db 18 GGAGAAGGGGGTGGTGC 1

RESULT 5

US-10-310-914A-1065883/c
; Sequence 1065883, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065883
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065883

Query Match 94.7%; Score 18; DB 11; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGC 18
|||||
Db 18 GGAGAAGGGGGTGGTGC 1

RESULT 6

US-10-310-914A-148924/c
; Sequence 148924, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148924
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148924

Query Match 84.2%; Score 16; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGT 16
|||||
Db 16 GGAGAAGGGGGTGGGT 1

RESULT 7

US-10-310-914A-129493
; Sequence 129493, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129493
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-129493

Query Match 83.2%; Score 15.8; DB 11; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.9e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 19
|||||
Db 1 GGAGAAGGGGGTGGTGCT 19

RESULT 8

US-10-310-914A-572030
; Sequence 572030, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 572030
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-572030

Query Match 83.2%; Score 15.8; DB 11; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.9e+03;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGTGCT 19
|||||
Db 1 GGAGAAGGGGGTGGTGCT 19

RESULT 9

US-10-310-914A-910792/c
; Sequence 910792, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910792
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910792

Query Match 83.2%; Score 15.8; DB 11; Length 22;

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Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 19 GGAGCAGGGGTGGGTCT 1

RESULT 10
US-10-310-914A-129473
; Sequence 129473, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129473
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-129473

Query Match 83.2%; Score 15.8; DB 11; Length 23;
Best Local Similarity 73.7%; Pred. No. 2.8e+03;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 2 GGAGGAGGGGAGGUGGCT 20

RESULT 11
US-10-310-914A-203215/c
; Sequence 203215, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203215
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203215

Query Match 83.2%; Score 15.8; DB 11; Length 23;
Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 22 GGGGAGGGGTGGGTGCT 4

RESULT 12
US-10-310-914A-203187/c
; Sequence 203187, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
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; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203187
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203187

Query Match 83.2%; Score 15.8; DB 11; Length 24;
Best Local Similarity 89.5%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTGCT 19
    ||||| ||||| ||||| |||||
Db 19 GGGGAGGGGTGGGTGCT 1

RESULT 13
US-10-310-914A-869326
; Sequence 869326, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 869326
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-869326

Query Match 81.1%; Score 15.4; DB 11; Length 18;
Best Local Similarity 82.4%; Pred. No. 4.4e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTGGGTG 17
    ||||| ||||| ||||| |||||
Db 1 GCGGAGGGGGGUGGUG 17

RESULT 14
US-10-310-914A-1065866/c
; Sequence 1065866, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065866
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065866

Query Match 78.9%; Score 15; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGG 15
    |||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 15
US-10-310-914A-148939/c
; Sequence 148939, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148939
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148939

Query Match 78.9%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGG 15
    |||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 16
US-10-310-914A-1065867/c
; Sequence 1065867, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1065867
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1065867

Query Match 78.9%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGG 15
    |||||
Db 15 GGAGAAGGGGTGGG 1

RESULT 17
US-10-310-914A-203240/c
; Sequence 203240, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
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; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203240

Query Match 77.9%; Score 14.8; DB 11; Length 19;
Best Local Similarity 88.9%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGAGAAGGGGTGGGTGC 18
    |||||
Db 18 GGGAAGGGGTGGGTGC 1

RESULT 18
US-10-310-914A-1058248
; Sequence 1058248, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1058248

Query Match 77.9%; Score 14.8; DB 11; Length 19;
Best Local Similarity 77.8%; Pred. No. 7.9e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 GAGAAGGGGTGGGTGCT 19
    |||||
Db 1 GAGAAGGGGTGGGTGCT 18

RESULT 19
US-10-310-914A-203210/c
; Sequence 203210, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203210
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-203210

Query Match 77.9%; Score 14.8; DB 11; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```



```
Qy      2 GAGAAGGGGTGGGTGCT 19
Db      20 GGAAGGGGTGGGTGCT 3

RESULT 20
US-10-310-914A-224190/c
; Sequence 224190, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224190
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-224190

Query Match      77.9%; Score 14.8; DB 11; Length 21;
Best Local Similarity 88.9%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAAGGGGTGGGTGCT 19
Db      19 GAGAAGGGGTGAGTGGT 2

RESULT 21
US-10-310-914A-910812/c
; Sequence 910812, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 910812
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-910812

Query Match      77.9%; Score 14.8; DB 11; Length 22;
Best Local Similarity 88.9%; Pred. No. 7.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GGAGAGGGGTGGGTGC 18
Db      18 GGAGAGGGGTGGGTTC 1

RESULT 22
US-11-060-756-184336
; Sequence 184336, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes

Qy      1 GGAGAGGGGTGGGTGC 18
Db      18 GGAGAGGGGTGGGTTC 1

US-11-060-756-184336
; Sequence 233127, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML01083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233127
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233127

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAAGGGGTGGGTGCT 19
Db      1 GAGAAGGGGTGAGTGGT 18

RESULT 23
US-11-060-756-223194
; Sequence 223194, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML01083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 223194
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-223194

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GAGAAGGGGTGGGTGCT 19
Db      5 GAGAAGGGGTGAGTGGT 22

RESULT 24
US-11-060-756-233127
; Sequence 233127, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AML01083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233127
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-233127

Query Match      77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


QY 2 GAGAGGGGGTGGTGCT 19
|||||
DB 4 GAGAGGGGGTGAGTGCT 21

RESULT 25

US-11-060-756-269887
; Sequence 269887, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269887

; LENGTH: 25
; TYPE: DNA

; ORGANISM: probe
US-11-060-756-269887

Query Match 77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
|||||
DB 2 GAGAGGGGGTGAGTGCT 19

RESULT 26

US-11-060-756-302280
; Sequence 302280, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 302280

; LENGTH: 25
; TYPE: DNA

; ORGANISM: probe
US-11-060-756-302280

Query Match 77.9%; Score 14.8; DB 13; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
|||||
DB 3 GAGAGGGGGTGAGTGCT 20

RESULT 27

US-10-310-914A-491217/c
; Sequence 491217, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 491217
; LENGTH: 18
; TYPE: RNA

; ORGANISM: Human
US-10-310-914A-491217

Query Match 75.8%; Score 14.4; DB 11; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGT 16
|||||
DB 16 GGAGAGGGGGTGGGT 1

RESULT 28

US-10-310-914A-224205/c
; Sequence 224205, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224205

; LENGTH: 19
; TYPE: RNA

; ORGANISM: Human
US-10-310-914A-224205

Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGGTG 17
|||||
DB 17 GAGAGGGGGTGAGTG 2

RESULT 29

US-10-310-914A-491213/c
; Sequence 491213, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 491213

; LENGTH: 19
; TYPE: RNA

; ORGANISM: Human
US-10-310-914A-491213

Query Match 75.8%; Score 14.4; DB 11; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAGGGGGTGGGT 16

```
Db      17  GGAGGAGGGGGTGGGT 2
||||| ||||| ||||| |||||
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289813
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-289813

Query Match      75.8%; Score 14.4; DB 11; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2  GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db      4  GAGAAGGGGGUGGUG 19

RESULT 33
US-10-310-914A-455081
; Sequence 455081, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 455081
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-455081

Query Match      75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2  GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db      9  GAGAAGGGGGUGGAG 24

RESULT 34
US-10-310-914A-856024
; Sequence 856024, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 856024
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-856024

Query Match      75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAGAGGGGGTGGGT 16
||||| ||||| ||||| |||||
; CURRENT APPLICATION NUMBER: US/10/310,914A
```

```
Db      17  GGAGGAGGGGGTGGGT 2
||||| ||||| ||||| |||||
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 289813
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-289813

Query Match      75.8%; Score 14.4; DB 11; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2  GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db      4  GAGAAGGGGGUGGUG 19

RESULT 33
US-10-310-914A-455081
; Sequence 455081, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 455081
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-455081

Query Match      75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2  GAGAAGGGGGTGGGTG 17
||||| ||||| ||||| |||||
Db      9  GAGAAGGGGGUGGAG 24

RESULT 34
US-10-310-914A-856024
; Sequence 856024, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 856024
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-856024

Query Match      75.8%; Score 14.4; DB 11; Length 24;
Best Local Similarity 81.2%; Pred. No. 1.2e+04;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAGAGGGGGTGGGT 16
||||| ||||| ||||| |||||
; CURRENT APPLICATION NUMBER: US/10/310,914A
```

Db 7 GGAGGAGGGGGUGGCU 22

RESULT 35

US-10-310-914A-986078/c
; Sequence 986078, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 986078

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-986078

Query Match 75.8%; Score 14.4; DB 11; Length 24;

Best Local Similarity 93.8%; Pred. No. 1.2e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGT 16

Db 20 GGACAAGGGGGTGGGT 5

RESULT 36

US-10-310-914A-939254
; Sequence 939254, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 939254

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-939254

Query Match 74.7%; Score 14.2; DB 11; Length 19;

Best Local Similarity 73.7%; Pred. No. 1.5e+04;

Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGAAGGGGGTGGGTGCT 19

Db 1 GGAGAGCGGGUGGGCGGU 19

RESULT 37

US-10-310-914A-1039501
; Sequence 1039501, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1039501

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1039501

Query Match

Best Local Similarity

Matches 15; Conservative

QY 1 GGAGAAGGGGGTGGGTGCT 19

Db 1 GGAGAAGGGGGCGCGGCU 19

RESULT 38

US-10-310-914A-1039502

; Sequence 1039502, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1039502

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1039502

Query Match

Best Local Similarity

Matches 15; Conservative

QY 1 GGAGAAGGGGGTGGGTGCT 19

Db 1 GGAGAAGGGGGCGGUGGCU 19

RESULT 39

US-10-310-914A-1051671

; Sequence 1051671, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1051671

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1051671

Query Match

Best Local Similarity

Matches 14; Conservative

QY 1 GGAGAAGGGGGTGGGTGCT 19

Db 1 GGAGGAGGAGGUGGAGGCU 19

```
RESULT 40
US-10-310-914A-1114392
; Sequence 1114392, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1114392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1114392

Query Match          74.7%; Score 14.2; DB 11; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.5e+04;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
||||| :||| :||| :||| :||| :
Db 1 GGAGAGGCGCTGGGUGCT 19

RESULT 41
US-10-310-914A-1151400
; Sequence 1151400, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1151400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1151400

Query Match          74.7%; Score 14.2; DB 11; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.5e+04;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
||||| :||| :||| :||| :||| :
Db 1 GGAGAGGCGCTGGGUGCT 19

RESULT 42
US-10-310-914A-649973/c
; Sequence 649973, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 649973
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-649973

Query Match          74.7%; Score 14.2; DB 11; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
||||| :||| :||| :||| :||| :
Db 20 GGAGCAGGCAGTGGGTGCT 2

RESULT 43
US-10-310-914A-1207983/c
; Sequence 1207983, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1207983
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1207983

Query Match          74.7%; Score 14.2; DB 11; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
||||| :||| :||| :||| :||| :
Db 20 GGAGCTGGGGTGGGAGCT 2

RESULT 44
US-10-310-914A-1112107/c
; Sequence 1112107, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1112107
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1112107

Query Match          74.7%; Score 14.2; DB 11; Length 22;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGAGAAGGGGTGGGTGCT 19
||||| :||| :||| :||| :||| :
Db 21 GGAGACGGGGTGACTGCT 3
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RESULT 45
US-11-121-849-35504
; Sequence 35504, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35504
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-35504

Query Match          74.7%; Score 14.2; DB 15; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGAAGGGGGTGGGTGCT 19
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Db 5 GGGGAAGGAGGTGGTGCT 23

RESULT 46
US-10-120-637A-27
; Sequence 27, Application US/10120637A
; Publication No. US20030134400A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
; FILE REFERENCE: 6804.US.P1
; CURRENT APPLICATION NUMBER: US/10/120,637A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 09/849,199
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' Nested Primer R01239
US-10-120-637A-27

Query Match          74.7%; Score 14.2; DB 7; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGAAGGGGGTGGGTGCT 19
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Db 2 GGAGCATGGGTAGGTGCT 20

RESULT 47
US-10-913-271-27
; Sequence 27, Application US/10913271
; Publication No. US20050003442A1
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; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
; FILE REFERENCE: 6804.US.P1
; CURRENT APPLICATION NUMBER: US/10/913,271
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/120,637
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 09/849,199
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' Nested Primer R01239
US-10-913-271-27

Query Match          74.7%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGAAGGGGGTGGGTGCT 19
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Db 2 GGAGCATGGGTAGGTGCT 20

RESULT 48
US-10-913-226-27
; Sequence 27, Application US/10913226
; Publication No. US20050005328A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
; FILE REFERENCE: 6804.US.P1
; CURRENT APPLICATION NUMBER: US/10/913,226
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/120,637
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 09/849,199
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' Nested Primer R01239
US-10-913-226-27

Query Match          74.7%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGAAGGGGGTGGGTGCT 19
   ||||| ||||| ||||| |||||
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Job time : 826 secs

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Db      2  GGAGCATGGGGTAGGTGCT 20

RESULT 49
US-10-913-779-27
; Sequence 27, Application US/10913779
; Publication No. US20050005329A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Thurmond, Jennifer M.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 6804.US.P1
; CURRENT APPLICATION NUMBER: US/10/913,779
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US/10/120,637
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 09/849,199
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' Nested Primer R01239
US-10-913-779-27

Query Match      74.7%; Score 14.2; DB 9; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGAGAGGGGGTGGTGCT 19
      ||||| ||||| ||||| |||||
Db      2  GGAGCATGGGGTAGGTGCT 20

RESULT 50
US-10-310-914A-479763
; Sequence 479763, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 479763
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-479763

Query Match      74.7%; Score 14.2; DB 11; Length 27;
Best Local Similarity 73.7%; Pred. No. 1.4e+04;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  GGAGAAGGGGGTGGTGCT 19
      ||||| ||||| ||||| |||||
Db      3  GGAGAUGUGGGUGGGGGCU 21

Search completed: October 14, 2006, 19:57:24
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2006, 19:44:42 ; Search time 122 Seconds
(without alignments)
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Title: US-10-604-926A-4539

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 3125932

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA New:*

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- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	14.2	74.7	30	6	US-10-477-471-7
2	13.8	72.6	21	9	US-11-320-440-213
3	13.2	69.5	18	7	US-11-370-584-9827
4	12.6	66.3	21	9	US-11-324-563-66
5	12.6	66.3	25	7	US-11-378-920-23
6	12.2	64.2	20	6	US-10-511-937-1926
7	12.2	64.2	22	6	US-10-548-681-35
8	12.2	64.2	25	8	US-11-217-529-60224
9	12.2	64.2	25	9	US-11-348-413-1052286
10	12.2	64.2	25	9	US-11-348-413-1052287
11	12.2	64.2	25	9	US-11-348-413-1052288
12	12.2	64.2	25	9	US-11-348-413-1052289
13	12.2	64.2	25	9	US-11-348-413-1052290
14	11.8	62.1	21	7	US-11-199-903-3
15	11.8	62.1	21	8	US-11-305-629-9
16	11.8	62.1	21	8	US-11-329-941-11
17	11.8	62.1	25	9	US-11-348-413-635553
18	11.8	62.1	25	9	US-11-348-413-709656
19	11.8	62.1	25	9	US-11-348-413-1052291
20	11.8	62.1	25	9	US-11-348-413-1052292
21	11.8	62.1	25	9	US-11-348-413-1236138
22	11.6	61.1	25	8	US-11-217-529-89292
23	11.6	61.1	25	9	US-11-348-413-69158

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Sequence 480500,	US-11-348-413-480500	25	61.1	11.6	25
Sequence 480501,	US-11-348-413-480501	25	61.1	11.6	26
Sequence 649751,	US-11-348-413-649751	25	61.1	11.6	27
Sequence 660009,	US-11-348-413-660009	25	61.1	11.6	28
Sequence 783470,	US-11-348-413-783470	25	61.1	11.6	29
Sequence 783471,	US-11-348-413-783471	25	61.1	11.6	30
Sequence 783472,	US-11-348-413-783472	25	61.1	11.6	31
Sequence 1225381,	US-11-348-413-1225381	27	61.1	11.6	32
Sequence 310, App	US-11-260-845-310	27	61.1	11.6	33
Sequence 179, App	US-11-368-233-179	28	61.1	11.6	34
Sequence 180, App	US-11-368-233-180	28	61.1	11.6	35
Sequence 4208, App	US-11-217-936-4208	19	60.0	11.4	36
Sequence 4466, App	US-11-217-936-4466	19	60.0	11.4	37
Sequence 25, Appl	US-11-316-132-25	20	60.0	11.4	38
Sequence 78, Appl	US-10-818-956-78	22	60.0	11.4	39
Sequence 380, App	US-11-317-660-380	22	60.0	11.4	40
Sequence 1139, App	US-11-317-660-1139	22	60.0	11.4	41
Sequence 94, Appl	US-11-242-139-94	22	60.0	11.4	42
Sequence 1462, App	US-11-283-550-1462	23	60.0	11.4	43
Sequence 1463, App	US-11-283-550-1463	23	60.0	11.4	44
Sequence 1464, App	US-11-283-550-1464	23	60.0	11.4	45
Sequence 1465, App	US-11-283-550-1465	23	60.0	11.4	46
Sequence 1466, App	US-11-283-550-1466	23	60.0	11.4	47
Sequence 1468, App	US-11-283-550-1468	23	60.0	11.4	48
Sequence 1469, App	US-11-283-550-1469	23	60.0	11.4	49
Sequence 1470, App	US-11-283-550-1470	23	60.0	11.4	50
Sequence 1471, App	US-11-283-550-1471	23	60.0	11.4	51
Sequence 1472, App	US-11-283-550-1472	23	60.0	11.4	52
Sequence 24, Appl	US-11-336-581-24	27	58.9	11.2	53
Sequence 3651, App	US-11-255-139A-3651	17	58.9	11.2	54
Sequence 2319, App	US-11-217-936-2319	19	58.9	11.2	55
Sequence 2614, App	US-11-217-936-2614	19	58.9	11.2	56
Sequence 9212, App	US-11-370-584-9212	20	58.9	11.2	57
Sequence 7, Appl	US-10-433-877-7	24	58.9	11.2	58
Sequence 33, Appl	US-11-440-877-33	24	58.9	11.2	59
Sequence 139293,	US-11-217-529-139293	25	58.9	11.2	60
Sequence 139294,	US-11-217-529-139294	25	58.9	11.2	61
Sequence 20662, A	US-11-348-413-20662	25	58.9	11.2	62
Sequence 20663, A	US-11-348-413-20663	25	58.9	11.2	63
Sequence 63430, A	US-11-348-413-63430	25	58.9	11.2	64
Sequence 63431, A	US-11-348-413-63431	25	58.9	11.2	65
Sequence 63432, A	US-11-348-413-63432	25	58.9	11.2	66
Sequence 63433, A	US-11-348-413-63433	25	58.9	11.2	67
Sequence 63434, A	US-11-348-413-63434	25	58.9	11.2	68
Sequence 63435, A	US-11-348-413-63435	25	58.9	11.2	69
Sequence 63436, A	US-11-348-413-63436	25	58.9	11.2	70
Sequence 63437, A	US-11-348-413-63437	25	58.9	11.2	71
Sequence 63438, A	US-11-348-413-63438	25	58.9	11.2	72
Sequence 176871,	US-11-348-413-176871	25	58.9	11.2	73
Sequence 325204,	US-11-348-413-325204	25	58.9	11.2	74
Sequence 325205,	US-11-348-413-325205	25	58.9	11.2	75
Sequence 487662,	US-11-348-413-487662	25	58.9	11.2	76
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Sequence 487664,	US-11-348-413-487664	25	58.9	11.2	78
Sequence 523014,	US-11-348-413-523014	25	58.9	11.2	79
Sequence 523015,	US-11-348-413-523015	25	58.9	11.2	80
Sequence 523016,	US-11-348-413-523016	25	58.9	11.2	81
Sequence 608020,	US-11-348-413-608020	25	58.9	11.2	82
Sequence 653807,	US-11-348-413-653807	25	58.9	11.2	83
Sequence 653808,	US-11-348-413-653808	25	58.9	11.2	84
Sequence 653809,	US-11-348-413-653809	25	58.9	11.2	85
Sequence 677939,	US-11-348-413-677939	25	58.9	11.2	86
Sequence 687440,	US-11-348-413-687440	25	58.9	11.2	87
Sequence 385, App	US-11-364-118-385	11	57.9	11	88
Sequence 76, Appl	US-11-158-209-76	11	57.9	11	89
Sequence 36, Appl	US-11-083-788-36	15	57.9	11	90
Sequence 1, Appl	US-11-348-506-1	19	57.9	11	91
Sequence 50, Appl	US-11-238-035-50	19	57.9	11	92
Sequence 20, Appl	US-10-519-069-20	22	57.9	11	93
Sequence 137, App	US-11-277-033-137	22	57.9	11	94
Sequence 32557, A	US-11-217-529-32557	25	57.9	11	95
		25	57.9	11	96

97	11	57.9	25	9	US-11-348-413-327661	Sequence 327661,	C 170	10.8	56.8	25	9	US-11-348-413-1218816	Sequence 1218816,
98	11	57.9	25	9	US-11-348-413-327662	Sequence 327662,	C 171	10.8	56.8	25	9	US-11-348-413-1218817	Sequence 1218817,
99	11	57.9	25	9	US-11-348-413-327663	Sequence 327663,	C 172	10.8	56.8	25	9	US-11-348-413-1218818	Sequence 1218818,
c 100	11	57.9	25	9	US-11-348-413-407486	Sequence 407486,	C 173	10.8	56.8	25	9	US-11-348-413-1218819	Sequence 1218819,
c 101	11	57.9	25	9	US-11-348-413-407487	Sequence 407487,	C 174	10.8	56.8	25	9	US-11-348-413-1218820	Sequence 1218820,
c 102	11	57.9	25	9	US-11-348-413-653045	Sequence 653045,	C 175	10.6	55.8	17	9	US-11-255-139A-7077	Sequence 7077, Ap
c 103	11	57.9	25	9	US-11-348-413-779269	Sequence 779269,	C 176	10.6	55.8	18	6	US-10-518-470-10	Sequence 10, Appl
c 104	11	57.9	25	9	US-11-348-413-779270	Sequence 779270,	C 177	10.6	55.8	18	6	US-11-321-421-147	Sequence 147, App
c 105	11	57.9	25	9	US-11-348-413-961173	Sequence 961173,	C 178	10.6	55.8	19	6	US-10-753-718-3414	Sequence 3414, Ap
c 106	11	57.9	25	9	US-11-348-413-1026218	Sequence 1026218,	C 179	10.6	55.8	20	6	US-10-525-116-1088	Sequence 1088, Ap
c 107	11	57.9	25	9	US-11-348-413-1270664	Sequence 1270664,	C 180	10.6	55.8	20	6	US-10-525-116-1089	Sequence 1089, Ap
c 108	11	57.9	27	6	US-10-858-013-51	Sequence 51, Appl	C 181	10.6	55.8	20	6	US-10-525-116-1092	Sequence 1092, Ap
c 109	11	57.9	27	6	US-10-858-013-803	Sequence 803, App	C 182	10.6	55.8	20	6	US-10-525-116-1093	Sequence 1093, Ap
c 110	11	57.9	27	6	US-10-858-164-51	Sequence 51, Appl	C 183	10.6	55.8	21	6	US-10-520-783-47	Sequence 47, Appl
c 111	11	57.9	27	6	US-10-858-164-803	Sequence 803, App	C 184	10.6	55.8	21	8	US-11-273-937-5	Sequence 5, Appl
c 112	11	57.9	30	6	US-10-723-683-146	Sequence 146, App	C 185	10.6	55.8	25	8	US-11-217-529-8812	Sequence 8812, Ap
c 113	11	57.9	30	6	US-10-522-341A-123	Sequence 123, App	C 186	10.6	55.8	25	8	US-11-217-529-21137	Sequence 21137, A
c 114	10.8	56.8	20	7	US-11-112-926-523	Sequence 523, App	C 187	10.6	55.8	25	8	US-11-217-529-21396	Sequence 21396, A
c 115	10.8	56.8	17	8	US-11-255-691-56	Sequence 56, Appl	C 188	10.6	55.8	25	8	US-11-217-529-21401	Sequence 21401, A
c 116	10.8	56.8	17	6	US-10-536-933-12	Sequence 12, Appl	C 189	10.6	55.8	25	8	US-11-217-529-21939	Sequence 21939, A
c 117	10.8	56.8	19	7	US-11-370-584-6862	Sequence 6862, Ap	C 190	10.6	55.8	25	8	US-11-217-529-29176	Sequence 29176, A
c 118	10.8	56.8	20	6	US-10-539-178-279	Sequence 279, App	C 191	10.6	55.8	25	8	US-11-217-529-29713	Sequence 29713, A
c 119	10.8	56.8	20	7	US-11-346-145-6	Sequence 6, Appl	C 192	10.6	55.8	25	8	US-11-217-529-47828	Sequence 47828, A
c 120	10.8	56.8	20	7	US-11-338-859-229	Sequence 229, App	C 193	10.6	55.8	25	8	US-11-217-529-56629	Sequence 56629, A
c 121	10.8	56.8	20	7	US-11-338-860-229	Sequence 229, App	C 194	10.6	55.8	25	8	US-11-217-529-87706	Sequence 87706, A
c 122	10.8	56.8	20	7	US-11-338-862-229	Sequence 229, App	C 195	10.6	55.8	25	8	US-11-217-529-132613	Sequence 132613,
c 123	10.8	56.8	20	7	US-11-338-864-229	Sequence 229, App	C 196	10.6	55.8	25	8	US-11-217-529-132635	Sequence 132635,
c 124	10.8	56.8	21	6	US-10-520-284-4	Sequence 4, Appl	C 197	10.6	55.8	25	8	US-11-217-529-143194	Sequence 143194,
c 125	10.8	56.8	23	6	US-10-858-013-18	Sequence 18, Appl	C 198	10.6	55.8	25	8	US-11-217-529-158897	Sequence 158897,
c 126	10.8	56.8	23	6	US-10-858-013-19	Sequence 19, Appl	C 199	10.6	55.8	25	8	US-11-217-529-165300	Sequence 165300,
c 127	10.8	56.8	23	6	US-10-858-164-18	Sequence 18, Appl	C 200	10.6	55.8	25	8	US-11-217-529-182632	Sequence 182632,
c 128	10.8	56.8	23	6	US-10-858-164-19	Sequence 19, Appl	C 201	10.6	55.8	25	8	US-11-217-529-182930	Sequence 182930,
c 129	10.8	56.8	24	6	US-10-502-993-8	Sequence 8, Appl	C 202	10.6	55.8	25	8	US-11-217-529-186594	Sequence 186594,
c 130	10.8	56.8	25	8	US-11-217-529-33528	Sequence 32528, A	C 203	10.6	55.8	25	8	US-11-322-523-17	Sequence 17, Appl
c 131	10.8	56.8	25	8	US-11-217-529-53557	Sequence 53557, A	C 204	10.6	55.8	25	9	US-11-348-413-38370	Sequence 38370, A
c 132	10.8	56.8	25	8	US-11-217-529-134506	Sequence 134506,	C 205	10.6	55.8	25	9	US-11-348-413-69159	Sequence 69159, A
c 133	10.8	56.8	25	8	US-11-217-529-155449	Sequence 155449,	C 206	10.6	55.8	25	9	US-11-348-413-90594	Sequence 90594, A
c 134	10.8	56.8	25	8	US-11-359-341-4	Sequence 4, Appl	C 207	10.6	55.8	25	9	US-11-348-413-90595	Sequence 90595, A
c 135	10.8	56.8	25	9	US-11-348-413-20660	Sequence 20660, A	C 208	10.6	55.8	25	9	US-11-348-413-90596	Sequence 90596, A
c 136	10.8	56.8	25	9	US-11-348-413-20661	Sequence 20661, A	C 209	10.6	55.8	25	9	US-11-348-413-90597	Sequence 90597, A
c 137	10.8	56.8	25	9	US-11-348-413-31367	Sequence 31367, A	C 210	10.6	55.8	25	9	US-11-348-413-90598	Sequence 90598, A
c 138	10.8	56.8	25	9	US-11-348-413-31368	Sequence 31368, A	C 211	10.6	55.8	25	9	US-11-348-413-90599	Sequence 90599, A
c 139	10.8	56.8	25	9	US-11-348-413-31369	Sequence 31369, A	C 212	10.6	55.8	25	9	US-11-348-413-90600	Sequence 90600, A
c 140	10.8	56.8	25	9	US-11-348-413-31370	Sequence 31370, A	C 213	10.6	55.8	25	9	US-11-348-413-168014	Sequence 168014,
c 141	10.8	56.8	25	9	US-11-348-413-31371	Sequence 31371, A	C 214	10.6	55.8	25	9	US-11-348-413-188055	Sequence 188055,
c 142	10.8	56.8	25	9	US-11-348-413-31372	Sequence 31372, A	C 215	10.6	55.8	25	9	US-11-348-413-188056	Sequence 188056,
c 143	10.8	56.8	25	9	US-11-348-413-63439	Sequence 63439, A	C 216	10.6	55.8	25	9	US-11-348-413-188057	Sequence 188057,
c 144	10.8	56.8	25	9	US-11-348-413-63440	Sequence 63440, A	C 217	10.6	55.8	25	9	US-11-348-413-188058	Sequence 188058,
c 145	10.8	56.8	25	9	US-11-348-413-475963	Sequence 475963,	C 218	10.6	55.8	25	9	US-11-348-413-192990	Sequence 192990,
c 146	10.8	56.8	25	9	US-11-348-413-475964	Sequence 475964,	C 219	10.6	55.8	25	9	US-11-348-413-192991	Sequence 192991,
c 147	10.8	56.8	25	9	US-11-348-413-475965	Sequence 475965,	C 220	10.6	55.8	25	9	US-11-348-413-192992	Sequence 192992,
c 148	10.8	56.8	25	9	US-11-348-413-475966	Sequence 475966,	C 221	10.6	55.8	25	9	US-11-348-413-192993	Sequence 192993,
c 149	10.8	56.8	25	9	US-11-348-413-487660	Sequence 487660,	C 222	10.6	55.8	25	9	US-11-348-413-198754	Sequence 198754,
c 150	10.8	56.8	25	9	US-11-348-413-487661	Sequence 487661,	C 223	10.6	55.8	25	9	US-11-348-413-198755	Sequence 198755,
c 151	10.8	56.8	25	9	US-11-348-413-523017	Sequence 523017,	C 224	10.6	55.8	25	9	US-11-348-413-198756	Sequence 198756,
c 152	10.8	56.8	25	9	US-11-348-413-523018	Sequence 523018,	C 225	10.6	55.8	25	9	US-11-348-413-198757	Sequence 198757,
c 153	10.8	56.8	25	9	US-11-348-413-876121	Sequence 876121,	C 226	10.6	55.8	25	9	US-11-348-413-231754	Sequence 231754,
c 154	10.8	56.8	25	9	US-11-348-413-1052293	Sequence 1052293,	C 227	10.6	55.8	25	9	US-11-348-413-231755	Sequence 231755,
c 155	10.8	56.8	25	9	US-11-348-413-1119188	Sequence 1119188,	C 228	10.6	55.8	25	9	US-11-348-413-231756	Sequence 231756,
c 156	10.8	56.8	25	9	US-11-348-413-1119189	Sequence 1119189,	C 229	10.6	55.8	25	9	US-11-348-413-231757	Sequence 231757,
c 157	10.8	56.8	25	9	US-11-348-413-1128016	Sequence 1128016,	C 230	10.6	55.8	25	9	US-11-348-413-407485	Sequence 407485,
c 158	10.8	56.8	25	9	US-11-348-413-1128017	Sequence 1128017,	C 231	10.6	55.8	25	9	US-11-348-413-475397	Sequence 475397,
c 159	10.8	56.8	25	9	US-11-348-413-1173660	Sequence 1173660,	C 232	10.6	55.8	25	9	US-11-348-413-475398	Sequence 475398,
c 160	10.8	56.8	25	9	US-11-348-413-1173661	Sequence 1173661,	C 233	10.6	55.8	25	9	US-11-348-413-475399	Sequence 475399,
c 161	10.8	56.8	25	9	US-11-348-413-1173662	Sequence 1173662,	C 234	10.6	55.8	25	9	US-11-348-413-475400	Sequence 475400,
c 162	10.8	56.8	25	9	US-11-348-413-1173663	Sequence 1173663,	C 235	10.6	55.8	25	9	US-11-348-413-475401	Sequence 475401,
c 163	10.8	56.8	25	9	US-11-348-413-1173664	Sequence 1173664,	C 236	10.6	55.8	25	9	US-11-348-413-475402	Sequence 475402,
c 164	10.8	56.8	25	9	US-11-348-413-1173665	Sequence 1173665,	C 237	10.6	55.8	25	9	US-11-348-413-475403	Sequence 475403,
c 165	10.8	56.8	25	9	US-11-348-413-1173666	Sequence 1173666,	C 238	10.6	55.8	25	9	US-11-348-413-475404	Sequence 475404,
c 166	10.8	56.8	25	9	US-11-348-413-1173667	Sequence 1173667,	C 239	10.6	55.8	25	9	US-11-348-413-475405	Sequence 475405,
c 167	10.8	56.8	25	9	US-11-348-413-1173668	Sequence 1173668,	C 240	10.6	55.8	25	9	US-11-348-413-475428	Sequence 475428,
c 168	10.8	56.8	25	9	US-11-348-413-1218813	Sequence 1218813,	C 241	10.6	55.8	25	9	US-11-348-413-475429	Sequence 475429,
c 169	10.8	56.8	25	9	US-11-348-413-1218814	Sequence 1218814,	C 242	10.6	55.8	25	9	US-11-348-413-475430	Sequence 475430,
c 170	10.8	56.8	25	9	US-11-348-413-1218815	Sequence 1218815,	C 243	10.6	55.8	25	9	US-11-348-413-475430	Sequence 475430,

243	10.6	55.8	25	9	US-11-348-413-475431	Sequence 475431,	316	10.4	54.7	25	9	US-11-348-413-786096	Sequence 786096,
244	10.6	55.8	25	9	US-11-348-413-475432	Sequence 475432,	317	10.4	54.7	25	9	US-11-348-413-830478	Sequence 830478,
245	10.6	55.8	25	9	US-11-348-413-475433	Sequence 475433,	318	10.4	54.7	25	9	US-11-348-413-876854	Sequence 876854,
246	10.6	55.8	25	9	US-11-348-413-475434	Sequence 475434,	c 319	10.4	54.7	25	9	US-11-348-413-885805	Sequence 885805,
247	10.6	55.8	25	9	US-11-348-413-480498	Sequence 480498,	c 320	10.4	54.7	25	9	US-11-348-413-983091	Sequence 983091,
248	10.6	55.8	25	9	US-11-348-413-607580	Sequence 607580,	c 321	10.4	54.7	25	9	US-11-348-413-996209	Sequence 996209,
c 249	10.6	55.8	25	9	US-11-348-413-626525	Sequence 626525,	c 322	10.4	54.7	25	9	US-11-348-413-1017547	Sequence 1017547,
250	10.6	55.8	25	9	US-11-348-413-641145	Sequence 641145,	c 323	10.4	54.7	25	9	US-11-348-413-1038624	Sequence 1038624,
251	10.6	55.8	25	9	US-11-348-413-675833	Sequence 675833,	c 324	10.4	54.7	25	9	US-11-348-413-1052294	Sequence 1052294,
252	10.6	55.8	25	9	US-11-348-413-681543	Sequence 681543,	c 325	10.4	54.7	25	9	US-11-348-413-1052295	Sequence 1052295,
c 253	10.6	55.8	25	9	US-11-348-413-783469	Sequence 783469,	c 326	10.4	54.7	25	9	US-11-348-413-1110649	Sequence 1110649,
254	10.6	55.8	25	9	US-11-348-413-789848	Sequence 789848,	c 327	10.4	54.7	25	9	US-11-348-413-1170764	Sequence 1170764,
c 255	10.6	55.8	25	9	US-11-348-413-795290	Sequence 795290,	c 328	10.4	54.7	25	9	US-11-348-413-1215918	Sequence 1215918,
c 256	10.6	55.8	25	9	US-11-348-413-795291	Sequence 795291,	c 329	10.4	54.7	25	9	US-11-348-413-1215919	Sequence 1215919,
c 257	10.6	55.8	25	9	US-11-348-413-795292	Sequence 795292,	c 330	10.4	54.7	25	9	US-11-348-413-1215920	Sequence 1215920,
c 258	10.6	55.8	25	9	US-11-348-413-795293	Sequence 795293,	c 331	10.2	53.7	17	6	US-10-516-032-23	Sequence 23, Appl
c 259	10.6	55.8	25	9	US-11-348-413-795294	Sequence 795294,	c 332	10.2	53.7	17	6	US-10-993-483A-86	Sequence 86, Appl
c 260	10.6	55.8	25	9	US-11-348-413-801793	Sequence 801793,	c 333	10.2	53.7	17	9	US-11-300-194-51	Sequence 51, Appl
c 261	10.6	55.8	25	9	US-11-348-413-801794	Sequence 801794,	c 334	10.2	53.7	17	9	US-11-255-139A-2329	Sequence 2329, Ap
c 262	10.6	55.8	25	9	US-11-348-413-801795	Sequence 801795,	c 335	10.2	53.7	17	9	US-11-255-139A-3652	Sequence 3652, Ap
c 263	10.6	55.8	25	9	US-11-348-413-801796	Sequence 801796,	c 336	10.2	53.7	18	7	US-11-340-574-46	Sequence 50, Appl
c 264	10.6	55.8	25	9	US-11-348-413-801797	Sequence 801797,	c 337	10.2	53.7	18	7	US-11-340-574-50	Sequence 50, Appl
c 265	10.6	55.8	25	9	US-11-348-413-801798	Sequence 801798,	c 338	10.2	53.7	18	7	US-11-370-584-7437	Sequence 7437, Ap
c 266	10.6	55.8	25	9	US-11-348-413-816512	Sequence 816512,	c 339	10.2	53.7	19	6	US-10-424-339-1375	Sequence 1375, Ap
c 267	10.6	55.8	25	9	US-11-348-413-844160	Sequence 844160,	c 340	10.2	53.7	19	6	US-10-424-339-1356	Sequence 1356, Ap
c 268	10.6	55.8	25	9	US-11-348-413-1061093	Sequence 1061093,	c 341	10.2	53.7	19	6	US-10-536-804-5	Sequence 5, Appl
c 269	10.6	55.8	25	9	US-11-348-413-1118424	Sequence 1118424,	c 342	10.2	53.7	19	6	US-10-881-580-65	Sequence 65, Appl
c 270	10.6	55.8	25	9	US-11-348-413-1118425	Sequence 1118425,	c 343	10.2	53.7	19	6	US-10-881-580-193	Sequence 193, Ap
c 271	10.6	55.8	25	9	US-11-348-413-1118426	Sequence 1118426,	c 344	10.2	53.7	19	6	US-10-825-485-167	Sequence 167, Ap
c 272	10.6	55.8	25	9	US-11-348-413-1118427	Sequence 1118427,	c 345	10.2	53.7	19	6	US-10-825-485-474	Sequence 474, Ap
c 273	10.6	55.8	25	9	US-11-348-413-1118428	Sequence 1118428,	c 346	10.2	53.7	19	6	US-10-753-718-528	Sequence 528, Ap
c 274	10.6	55.8	25	9	US-11-348-413-1118429	Sequence 1118429,	c 347	10.2	53.7	19	7	US-11-318-240-11	Sequence 11, Appl
c 275	10.6	55.8	25	9	US-11-348-413-1118430	Sequence 1118430,	c 348	10.2	53.7	19	8	US-11-251-465-591	Sequence 591, Ap
c 276	10.6	55.8	25	9	US-11-348-413-1118431	Sequence 1118431,	c 349	10.2	53.7	19	8	US-11-219-582A-23	Sequence 23, Appl
c 277	10.6	55.8	25	9	US-11-348-413-1118432	Sequence 1118432,	c 350	10.2	53.7	19	8	US-11-219-582A-25	Sequence 25, Appl
c 278	10.6	55.8	25	9	US-11-348-413-1124401	Sequence 1124401,	c 351	10.2	53.7	19	8	US-11-219-582A-27	Sequence 27, Appl
c 279	10.6	55.8	26	6	US-10-511-937-2158	Sequence 2158, Ap	c 352	10.2	53.7	19	8	US-11-219-582A-31	Sequence 31, Appl
c 280	10.6	55.8	26	6	US-11-350-336-26	Sequence 26, Appl	c 353	10.2	53.7	19	8	US-11-219-582A-39	Sequence 39, Appl
c 281	10.6	55.8	27	6	US-10-858-013-946	Sequence 946, Appl	c 354	10.2	53.7	19	8	US-11-219-582A-43	Sequence 43, Appl
c 282	10.6	55.8	27	6	US-10-858-013-947	Sequence 947, Appl	c 355	10.2	53.7	19	8	US-11-219-582A-45	Sequence 45, Appl
c 283	10.6	55.8	27	6	US-10-858-164-946	Sequence 946, Appl	c 356	10.2	53.7	19	8	US-11-219-582A-47	Sequence 47, Appl
c 284	10.6	55.8	27	6	US-10-858-164-947	Sequence 947, Appl	c 357	10.2	53.7	19	8	US-11-219-582A-25	Sequence 25, Appl
c 285	10.6	55.8	29	7	US-11-395-249-204	Sequence 204, Appl	c 358	10.2	53.7	19	9	US-11-219-625A-25	Sequence 25, Appl
c 286	10.6	55.8	29	7	US-11-133-075-76	Sequence 76, Appl	c 359	10.2	53.7	19	9	US-11-219-625A-26	Sequence 26, Appl
c 287	10.6	55.8	30	9	US-11-036-257-153	Sequence 153, Appl	c 360	10.2	53.7	19	9	US-11-217-936-2950	Sequence 2950, Ap
c 288	10.4	54.7	18	7	US-11-370-584-7812	Sequence 7812, Ap	c 361	10.2	53.7	19	9	US-11-217-936-3177	Sequence 3177, Ap
c 289	10.4	54.7	18	8	US-11-293-697-5452	Sequence 5452, Ap	c 362	10.2	53.7	19	9	US-11-361-793-25	Sequence 25, Appl
c 290	10.4	54.7	19	9	US-11-217-936-425	Sequence 425, Appl	c 363	10.2	53.7	19	9	US-11-361-793-26	Sequence 26, Appl
c 291	10.4	54.7	19	9	US-11-217-936-535	Sequence 535, Appl	c 364	10.2	53.7	20	6	US-10-511-937-679	Sequence 679, Appl
c 292	10.4	54.7	19	9	US-11-294-621-109	Sequence 109, Appl	c 365	10.2	53.7	20	6	US-10-517-441-1027	Sequence 1027, Ap
c 293	10.4	54.7	20	8	US-11-189-597-8	Sequence 8, Appl	c 366	10.2	53.7	20	6	US-10-525-116-982	Sequence 982, Ap
c 294	10.4	54.7	20	8	US-11-301-764-125	Sequence 125, Appl	c 367	10.2	53.7	20	6	US-10-525-116-1080	Sequence 1080, Ap
c 295	10.4	54.7	23	8	US-11-283-550-1461	Sequence 1461, Appl	c 368	10.2	53.7	20	7	US-11-370-584-5435	Sequence 5435, Ap
c 296	10.4	54.7	23	8	US-11-283-550-1473	Sequence 1473, Ap	c 369	10.2	53.7	20	7	US-11-370-584-5858	Sequence 5858, Ap
c 297	10.4	54.7	25	8	US-11-217-529-11019	Sequence 11019, A	c 370	10.2	53.7	20	7	US-11-370-584-5972	Sequence 5972, Ap
c 298	10.4	54.7	25	8	US-11-217-529-16737	Sequence 16737, A	c 371	10.2	53.7	20	7	US-11-370-584-7145	Sequence 7145, Ap
c 299	10.4	54.7	25	8	US-11-217-529-56574	Sequence 56574, A	c 372	10.2	53.7	20	7	US-11-370-584-10500	Sequence 10500, A
c 300	10.4	54.7	25	8	US-11-217-529-60077	Sequence 60077, A	c 373	10.2	53.7	20	9	US-11-293-598-14	Sequence 14, Appl
c 301	10.4	54.7	25	8	US-11-217-529-92657	Sequence 92657, A	c 374	10.2	53.7	20	9	US-11-207-382-153	Sequence 153, Appl
c 302	10.4	54.7	25	8	US-11-217-529-113705	Sequence 113705,	c 375	10.2	53.7	21	6	US-10-517-441-841	Sequence 841, Appl
c 303	10.4	54.7	25	8	US-11-348-413-177636	Sequence 177636,	c 376	10.2	53.7	21	6	US-10-997-086-28	Sequence 28, Appl
c 304	10.4	54.7	25	9	US-11-348-413-177637	Sequence 177637,	c 377	10.2	53.7	21	6	US-10-641-321-158	Sequence 158, Appl
c 305	10.4	54.7	25	9	US-11-348-413-177638	Sequence 177638,	c 378	10.2	53.7	21	8	US-11-251-465-592	Sequence 592, Ap
c 306	10.4	54.7	25	9	US-11-348-413-177639	Sequence 177639,	c 379	10.2	53.7	21	9	US-11-219-625A-23	Sequence 23, Appl
c 307	10.4	54.7	25	9	US-11-348-413-271160	Sequence 271160,	c 380	10.2	53.7	21	9	US-11-219-625A-24	Sequence 24, Appl
c 308	10.4	54.7	25	9	US-11-348-413-271161	Sequence 271161,	c 381	10.2	53.7	21	9	US-11-219-625A-27	Sequence 27, Appl
c 309	10.4	54.7	25	9	US-11-348-413-271162	Sequence 271162,	c 382	10.2	53.7	21	9	US-11-219-625A-28	Sequence 28, Appl
c 310	10.4	54.7	25	9	US-11-348-413-569752	Sequence 569752,	c 383	10.2	53.7	21	9	US-11-219-625A-29	Sequence 29, Appl
c 311	10.4	54.7	25	9	US-11-348-413-612339	Sequence 612339,	c 384	10.2	53.7	21	9	US-11-219-625A-30	Sequence 30, Appl
c 312	10.4	54.7	25	9	US-11-348-413-695154	Sequence 695154,	c 385	10.2	53.7	21	9	US-11-219-625A-31	Sequence 31, Appl
c 313	10.4	54.7	25	9	US-11-348-413-784243	Sequence 784243,	c 386	10.2	53.7	21	9	US-11-219-625A-32	Sequence 32, Appl
c 314	10.4	54.7	25	9	US-11-348-413-784244	Sequence 784244,	c 387	10.2	53.7	21	9	US-11-219-625A-39	Sequence 39, Appl
c 315	10.4	54.7	25	9	US-11-348-413-784245	Sequence 784245,	c 388	10.2	53.7	21	9	US-11-219-625A-40	Sequence 40, Appl

c 389	10.2	53.7	21	9	US-11-219-625A-43	Sequence 43, Appl	462	10.2	53.7	25	9	US-11-348-413-104405	Sequence 104405,
c 390	10.2	53.7	21	9	US-11-219-625A-44	Sequence 44, Appl	463	10.2	53.7	25	9	US-11-348-413-104406	Sequence 104406,
c 391	10.2	53.7	21	9	US-11-219-625A-45	Sequence 45, Appl	464	10.2	53.7	25	9	US-11-348-413-104407	Sequence 104407,
c 392	10.2	53.7	21	9	US-11-219-625A-46	Sequence 46, Appl	465	10.2	53.7	25	9	US-11-348-413-104408	Sequence 104408,
c 393	10.2	53.7	21	9	US-11-219-625A-47	Sequence 47, Appl	c 466	10.2	53.7	25	9	US-11-348-413-136541	Sequence 136541,
c 394	10.2	53.7	21	9	US-11-219-625A-48	Sequence 48, Appl	c 467	10.2	53.7	25	9	US-11-348-413-136542	Sequence 136542,
c 395	10.2	53.7	21	9	US-11-361-793-23	Sequence 23, Appl	c 468	10.2	53.7	25	9	US-11-348-413-158643	Sequence 158643,
c 396	10.2	53.7	21	9	US-11-361-793-24	Sequence 24, Appl	469	10.2	53.7	25	9	US-11-348-413-158644	Sequence 158644,
c 397	10.2	53.7	21	9	US-11-361-793-27	Sequence 27, Appl	c 470	10.2	53.7	25	9	US-11-348-413-176872	Sequence 176872,
c 398	10.2	53.7	21	9	US-11-361-793-28	Sequence 28, Appl	471	10.2	53.7	25	9	US-11-348-413-185521	Sequence 185521,
c 399	10.2	53.7	21	9	US-11-361-793-29	Sequence 29, Appl	472	10.2	53.7	25	9	US-11-348-413-185522	Sequence 185522,
c 400	10.2	53.7	21	9	US-11-361-793-30	Sequence 30, Appl	473	10.2	53.7	25	9	US-11-348-413-185523	Sequence 185523,
c 401	10.2	53.7	21	9	US-11-361-793-31	Sequence 31, Appl	474	10.2	53.7	25	9	US-11-348-413-185524	Sequence 185524,
c 402	10.2	53.7	21	9	US-11-361-793-32	Sequence 32, Appl	475	10.2	53.7	25	9	US-11-348-413-185525	Sequence 185525,
c 403	10.2	53.7	21	9	US-11-361-793-33	Sequence 33, Appl	476	10.2	53.7	25	9	US-11-348-413-185526	Sequence 185526,
c 404	10.2	53.7	21	9	US-11-361-793-39	Sequence 39, Appl	477	10.2	53.7	25	9	US-11-348-413-185527	Sequence 185527,
c 405	10.2	53.7	21	9	US-11-361-793-40	Sequence 40, Appl	478	10.2	53.7	25	9	US-11-348-413-185528	Sequence 185528,
c 406	10.2	53.7	21	9	US-11-361-793-43	Sequence 43, Appl	479	10.2	53.7	25	9	US-11-348-413-199968	Sequence 199968,
c 407	10.2	53.7	21	9	US-11-361-793-44	Sequence 44, Appl	480	10.2	53.7	25	9	US-11-348-413-199969	Sequence 199969,
c 408	10.2	53.7	21	9	US-11-361-793-45	Sequence 45, Appl	481	10.2	53.7	25	9	US-11-348-413-199970	Sequence 199970,
c 409	10.2	53.7	21	9	US-11-361-793-47	Sequence 47, Appl	482	10.2	53.7	25	9	US-11-348-413-213902	Sequence 213902,
c 410	10.2	53.7	21	9	US-11-361-793-48	Sequence 48, Appl	483	10.2	53.7	25	9	US-11-348-413-213903	Sequence 213903,
c 411	10.2	53.7	22	6	US-10-526-905-31	Sequence 31, Appl	484	10.2	53.7	25	9	US-11-348-413-213904	Sequence 213904,
c 412	10.2	53.7	22	6	US-10-526-905-31	Sequence 31, Appl	485	10.2	53.7	25	9	US-11-348-413-213905	Sequence 213905,
c 413	10.2	53.7	22	7	US-10-107-746-3	Sequence 196, App	486	10.2	53.7	25	9	US-11-348-413-220778	Sequence 220778,
c 414	10.2	53.7	23	7	US-11-340-080-81	Sequence 81, Appl	487	10.2	53.7	25	9	US-11-348-413-220779	Sequence 220779,
c 415	10.2	53.7	23	7	US-11-340-080-82	Sequence 82, Appl	488	10.2	53.7	25	9	US-11-348-413-220780	Sequence 220780,
c 416	10.2	53.7	23	7	US-11-340-080-83	Sequence 83, Appl	c 490	10.2	53.7	25	9	US-11-348-413-324244	Sequence 324244,
c 417	10.2	53.7	23	7	US-11-340-080-84	Sequence 84, Appl	c 491	10.2	53.7	25	9	US-11-348-413-324245	Sequence 324245,
c 418	10.2	53.7	23	7	US-11-340-080-85	Sequence 85, Appl	c 492	10.2	53.7	25	9	US-11-348-413-324246	Sequence 324246,
c 419	10.2	53.7	23	7	US-11-340-080-86	Sequence 86, Appl	c 493	10.2	53.7	25	9	US-11-348-413-324247	Sequence 324247,
c 420	10.2	53.7	23	7	US-11-340-080-87	Sequence 87, Appl	c 494	10.2	53.7	25	9	US-11-348-413-324248	Sequence 324248,
c 421	10.2	53.7	23	7	US-11-340-080-88	Sequence 88, Appl	c 495	10.2	53.7	25	9	US-11-348-413-324249	Sequence 324249,
c 422	10.2	53.7	23	7	US-11-340-080-89	Sequence 89, Appl	c 496	10.2	53.7	25	9	US-11-348-413-324250	Sequence 324250,
c 423	10.2	53.7	23	8	US-11-078-073-81	Sequence 81, Appl	c 497	10.2	53.7	25	9	US-11-348-413-324251	Sequence 324251,
c 424	10.2	53.7	23	8	US-11-078-073-82	Sequence 82, Appl	c 498	10.2	53.7	25	9	US-11-348-413-324252	Sequence 324252,
c 425	10.2	53.7	23	8	US-11-078-073-83	Sequence 83, Appl	c 499	10.2	53.7	25	9	US-11-348-413-344067	Sequence 344067,
c 426	10.2	53.7	23	8	US-11-078-073-84	Sequence 84, Appl	c 500	10.2	53.7	25	9	US-11-348-413-344068	Sequence 344068,
c 427	10.2	53.7	23	8	US-11-078-073-85	Sequence 85, Appl	c 501	10.2	53.7	25	9	US-11-348-413-348889	Sequence 348889,
c 428	10.2	53.7	23	8	US-11-078-073-86	Sequence 86, Appl	502	10.2	53.7	25	9	US-11-348-413-348890	Sequence 348890,
c 429	10.2	53.7	23	8	US-11-078-073-87	Sequence 87, Appl	503	10.2	53.7	25	9	US-11-348-413-390676	Sequence 390676,
c 430	10.2	53.7	23	8	US-11-078-073-88	Sequence 88, Appl	504	10.2	53.7	25	9	US-11-348-413-410811	Sequence 410811,
c 431	10.2	53.7	23	8	US-11-078-073-89	Sequence 89, Appl	505	10.2	53.7	25	9	US-11-348-413-410812	Sequence 410812,
c 432	10.2	53.7	24	7	US-11-095-042-7	Sequence 7, Appli	506	10.2	53.7	25	9	US-11-348-413-410813	Sequence 410813,
c 433	10.2	53.7	25	6	US-10-915-763A-10	Sequence 10, Appl	507	10.2	53.7	25	9	US-11-348-413-410814	Sequence 410814,
c 434	10.2	53.7	25	6	US-10-354-933-1011	Sequence 1011, App	508	10.2	53.7	25	9	US-11-348-413-410815	Sequence 410815,
c 435	10.2	53.7	25	7	US-11-234-676-179	Sequence 179, App	509	10.2	53.7	25	9	US-11-348-413-585315	Sequence 585315,
c 436	10.2	53.7	25	8	US-11-217-529-24718	Sequence 24718, A	510	10.2	53.7	25	9	US-11-348-413-585316	Sequence 585316,
c 437	10.2	53.7	25	8	US-11-217-529-24723	Sequence 24723, A	c 511	10.2	53.7	25	9	US-11-348-413-589373	Sequence 589373,
c 438	10.2	53.7	25	8	US-11-217-529-27814	Sequence 27814, A	c 512	10.2	53.7	25	9	US-11-348-413-589374	Sequence 589374,
c 439	10.2	53.7	25	8	US-11-217-529-30334	Sequence 30334, A	c 513	10.2	53.7	25	9	US-11-348-413-592998	Sequence 592998,
c 440	10.2	53.7	25	8	US-11-217-529-36261	Sequence 36261, A	514	10.2	53.7	25	9	US-11-348-413-592999	Sequence 592999,
c 441	10.2	53.7	25	8	US-11-217-529-41137	Sequence 41137, A	515	10.2	53.7	25	9	US-11-348-413-593000	Sequence 593000,
c 442	10.2	53.7	25	8	US-11-217-529-46756	Sequence 46756, A	516	10.2	53.7	25	9	US-11-348-413-593001	Sequence 593001,
c 443	10.2	53.7	25	8	US-11-217-529-56599	Sequence 56599, A	517	10.2	53.7	25	9	US-11-348-413-593002	Sequence 593002,
c 444	10.2	53.7	25	8	US-11-217-529-93817	Sequence 93817, A	518	10.2	53.7	25	9	US-11-348-413-610218	Sequence 610218,
c 445	10.2	53.7	25	8	US-11-217-529-104158	Sequence 104158, A	519	10.2	53.7	25	9	US-11-348-413-611866	Sequence 611866,
c 446	10.2	53.7	25	8	US-11-217-529-115602	Sequence 115602, A	520	10.2	53.7	25	9	US-11-348-413-614787	Sequence 614787,
c 447	10.2	53.7	25	8	US-11-217-529-122010	Sequence 122010, A	521	10.2	53.7	25	9	US-11-348-413-650873	Sequence 650873,
c 448	10.2	53.7	25	8	US-11-217-529-142300	Sequence 142300, A	522	10.2	53.7	25	9	US-11-348-413-655630	Sequence 655630,
c 449	10.2	53.7	25	8	US-11-217-529-145931	Sequence 145931, A	523	10.2	53.7	25	9	US-11-348-413-679840	Sequence 679840,
c 450	10.2	53.7	25	8	US-11-217-529-163015	Sequence 163015, A	524	10.2	53.7	25	9	US-11-348-413-681526	Sequence 681526,
c 451	10.2	53.7	25	9	US-11-348-413-22794	Sequence 22794, A	525	10.2	53.7	25	9	US-11-348-413-696113	Sequence 696113,
c 452	10.2	53.7	25	9	US-11-348-413-22795	Sequence 22795, A	526	10.2	53.7	25	9	US-11-348-413-703158	Sequence 703158,
c 453	10.2	53.7	25	9	US-11-348-413-22796	Sequence 22796, A	527	10.2	53.7	25	9	US-11-348-413-703158	Sequence 703158,
c 454	10.2	53.7	25	9	US-11-348-413-22797	Sequence 22797, A	528	10.2	53.7	25	9	US-11-348-413-780621	Sequence 780621,
c 455	10.2	53.7	25	9	US-11-348-413-22798	Sequence 22798, A	529	10.2	53.7	25	9	US-11-348-413-790424	Sequence 790424,
c 456	10.2	53.7	25	9	US-11-348-413-24417	Sequence 24417, A	530	10.2	53.7	25	9	US-11-348-413-792471	Sequence 792471,
c 457	10.2	53.7	25	9	US-11-348-413-27745	Sequence 27745, A	531	10.2	53.7	25	9	US-11-348-413-792472	Sequence 792472,
c 458	10.2	53.7	25	9	US-11-348-413-63429	Sequence 63429, A	532	10.2	53.7	25	9	US-11-348-413-792473	Sequence 792473,
c 459	10.2	53.7	25	9	US-11-348-413-71712	Sequence 71712, A	533	10.2	53.7	25	9	US-11-348-413-830049	Sequence 830049,
c 460	10.2	53.7	25	9	US-11-348-413-104403	Sequence 104403, A	534	10.2	53.7	25	9	US-11-348-413-830049	Sequence 830049,
c 461	10.2	53.7	25	9	US-11-348-413-104404	Sequence 104404, A	534	10.2	53.7	25	9	US-11-348-413-832774	Sequence 832774,

535	10.2	53.7	25	9	US-11-348-413-857332	Sequence 857332,	608	10	52.6	21	7	US-11-260-845-181	Sequence 181, App
536	10.2	53.7	25	9	US-11-348-413-874104	Sequence 874104,	609	10	52.6	21	7	US-11-260-845-186	Sequence 186, App
c 537	10.2	53.7	25	9	US-11-348-413-880485	Sequence 880485,	610	10	52.6	21	7	US-11-259-588-86	Sequence 86, Appl
c 538	10.2	53.7	25	9	US-11-348-413-957149	Sequence 957149,	c 611	10	52.6	21	7	US-11-084-700-121	Sequence 121, App
c 539	10.2	53.7	25	9	US-11-348-413-968628	Sequence 968628,	c 612	10	52.6	21	7	US-11-112-926-550	Sequence 550, App
c 540	10.2	53.7	25	9	US-11-348-413-985909	Sequence 985909,	c 613	10	52.6	21	9	US-11-320-440-202	Sequence 202, App
c 541	10.2	53.7	25	9	US-11-348-413-985910	Sequence 985910,	614	10	52.6	22	7	US-11-260-845-182	Sequence 182, App
c 542	10.2	53.7	25	9	US-11-348-413-995220	Sequence 995220,	615	10	52.6	22	7	US-11-389-343-794	Sequence 794, App
c 543	10.2	53.7	25	9	US-11-348-413-102706	Sequence 102706,	616	10	52.6	22	8	US-11-298-875A-61	Sequence 61, Appl
c 544	10.2	53.7	25	9	US-11-348-413-1051169	Sequence 1051169,	617	10	52.6	22	8	US-11-254-524-20	Sequence 20, Appl
c 545	10.2	53.7	25	9	US-11-348-413-1052285	Sequence 1052285,	c 618	10	52.6	23	8	US-11-283-550-1474	Sequence 1474, Ap
c 546	10.2	53.7	25	9	US-11-348-413-1124402	Sequence 1124402,	c 619	10	52.6	23	8	US-11-283-550-1475	Sequence 1475, Ap
c 547	10.2	53.7	25	9	US-11-348-413-1129371	Sequence 1129371,	c 620	10	52.6	23	8	US-11-283-550-5260	Sequence 5260, Ap
c 548	10.2	53.7	25	9	US-11-348-413-1129372	Sequence 1129372,	621	10	52.6	23	8	US-11-283-550-5261	Sequence 5261, Ap
c 549	10.2	53.7	25	9	US-11-348-413-1129373	Sequence 1129373,	622	10	52.6	23	8	US-11-283-550-5262	Sequence 5262, Ap
c 550	10.2	53.7	25	9	US-11-348-413-1160700	Sequence 1160700,	623	10	52.6	23	8	US-11-283-550-5263	Sequence 5263, Ap
c 551	10.2	53.7	25	9	US-11-348-413-1205861	Sequence 1205861,	624	10	52.6	23	8	US-11-283-550-5264	Sequence 5264, Ap
c 552	10.2	53.7	25	9	US-11-348-413-1205862	Sequence 1205862,	625	10	52.6	23	8	US-11-283-550-5265	Sequence 5265, Ap
c 553	10.2	53.7	25	9	US-11-348-413-1226558	Sequence 1226558,	c 626	10	52.6	24	6	US-10-858-013-184	Sequence 184, App
c 554	10.2	53.7	25	9	US-11-348-413-1253325	Sequence 1253325,	c 627	10	52.6	24	6	US-10-858-013-185	Sequence 185, App
c 555	10.2	53.7	25	9	US-11-348-413-1263368	Sequence 1263368,	c 628	10	52.6	24	6	US-10-858-013-186	Sequence 186, App
c 556	10.2	53.7	25	9	US-11-348-413-1263369	Sequence 1263369,	c 629	10	52.6	24	6	US-10-466-817-1	Sequence 1, Appli
c 557	10.2	53.7	25	9	US-11-348-413-1266309	Sequence 1266309,	c 630	10	52.6	24	6	US-10-858-164-184	Sequence 184, App
c 558	10.2	53.7	25	6	US-10-552-552-20	Sequence 20, Appl	c 631	10	52.6	24	6	US-10-858-164-185	Sequence 185, App
c 559	10.2	53.7	26	8	US-11-173-889-51	Sequence 51, Appl	c 632	10	52.6	24	6	US-10-858-164-186	Sequence 186, App
c 560	10.2	53.7	26	8	US-11-173-889-63	Sequence 63, Appl	c 633	10	52.6	24	6	US-10-888-359B-85	Sequence 85, Appl
c 561	10.2	53.7	26	8	US-11-173-889-78	Sequence 78, Appl	c 634	10	52.6	24	9	US-11-293-558-37	Sequence 37, Appl
c 562	10.2	53.7	27	8	US-11-200-465-5	Sequence 5, Appli	c 635	10	52.6	25	8	US-11-217-529-14012	Sequence 14012, A
c 563	10.2	53.7	27	8	US-11-223-812-5	Sequence 5, Appli	c 636	10	52.6	25	8	US-11-217-529-22553	Sequence 22553, A
c 564	10.2	53.7	28	7	US-11-234-676-193	Sequence 193, App	c 637	10	52.6	25	8	US-11-217-529-34937	Sequence 34937, A
c 565	10.2	53.7	29	9	US-11-372-250-2	Sequence 2, Appli	c 638	10	52.6	25	8	US-11-217-529-39671	Sequence 39671, A
c 566	10.2	53.7	30	8	US-11-234-676-180	Sequence 180, App	c 639	10	52.6	25	8	US-11-217-529-67056	Sequence 67056, A
c 567	10.2	53.7	30	8	US-11-238-155-29	Sequence 29, Appl	c 640	10	52.6	25	8	US-11-217-529-67117	Sequence 67117, A
c 568	10.2	53.7	30	8	US-11-238-155-35	Sequence 35, Appl	c 641	10	52.6	25	8	US-11-217-529-83862	Sequence 83862, A
c 569	10.2	53.7	30	8	US-11-238-155-37	Sequence 37, Appl	c 642	10	52.6	25	8	US-11-217-529-84700	Sequence 84700, A
c 570	10.2	53.7	30	8	US-11-238-155-39	Sequence 39, Appl	c 643	10	52.6	25	8	US-11-217-529-85590	Sequence 85590, A
c 571	10.2	53.7	30	8	US-11-238-155-41	Sequence 41, Appl	c 644	10	52.6	25	8	US-11-217-529-97073	Sequence 97073, A
c 572	10	52.6	15	7	US-11-342-392-3	Sequence 3, Appli	c 645	10	52.6	25	8	US-11-217-529-98349	Sequence 98349, A
c 573	10	52.6	15	7	US-11-083-788-92	Sequence 92, Appl	c 646	10	52.6	25	8	US-11-217-529-110422	Sequence 110422, A
c 574	10	52.6	18	7	US-11-370-584-6722	Sequence 6722, Ap	c 647	10	52.6	25	8	US-11-217-529-111944	Sequence 111944, A
c 575	10	52.6	19	6	US-10-424-339-781	Sequence 781, App	c 648	10	52.6	25	8	US-11-217-529-113380	Sequence 113380, A
c 576	10	52.6	19	6	US-10-424-339-990	Sequence 990, App	c 649	10	52.6	25	8	US-11-217-529-119328	Sequence 119328, A
c 577	10	52.6	19	7	US-11-091-000-15	Sequence 15, Appl	c 650	10	52.6	25	8	US-11-217-529-119321	Sequence 119321, A
c 578	10	52.6	19	7	US-11-299-391-253	Sequence 253, App	c 651	10	52.6	25	8	US-11-217-529-127535	Sequence 127535, A
c 579	10	52.6	19	7	US-11-299-391-680	Sequence 680, App	c 652	10	52.6	25	8	US-11-217-529-127537	Sequence 127537, A
c 580	10	52.6	19	7	US-11-299-391-931	Sequence 931, App	c 653	10	52.6	25	8	US-11-217-529-127555	Sequence 127555, A
c 581	10	52.6	19	7	US-11-299-391-1255	Sequence 1255, Ap	c 654	10	52.6	25	8	US-11-217-529-140697	Sequence 140697, A
c 582	10	52.6	19	8	US-11-258-360-21	Sequence 21, Appl	c 655	10	52.6	25	8	US-11-217-529-161103	Sequence 161103, A
c 583	10	52.6	19	9	US-11-217-936-2079	Sequence 2079, Ap	c 656	10	52.6	25	8	US-11-217-529-176787	Sequence 176787, A
c 584	10	52.6	19	9	US-11-217-936-2374	Sequence 2374, Ap	c 657	10	52.6	25	8	US-11-217-529-176792	Sequence 176792, A
c 585	10	52.6	19	9	US-11-217-936-4156	Sequence 4156, Ap	c 658	10	52.6	25	8	US-11-217-529-176795	Sequence 176795, A
c 586	10	52.6	19	9	US-11-217-936-4414	Sequence 4414, Ap	c 659	10	52.6	25	8	US-11-217-529-184124	Sequence 184124, A
c 587	10	52.6	19	9	US-11-102-087-1668	Sequence 1668, Ap	c 660	10	52.6	25	8	US-11-217-529-184131	Sequence 184131, A
c 588	10	52.6	20	6	US-10-511-455-83	Sequence 83, Appl	c 661	10	52.6	25	8	US-11-217-529-185662	Sequence 185662, A
c 589	10	52.6	20	6	US-10-559-415-107	Sequence 107, App	c 662	10	52.6	25	8	US-11-217-529-185663	Sequence 185663, A
c 590	10	52.6	20	6	US-10-668-050-105	Sequence 105, App	c 663	10	52.6	25	8	US-11-217-529-185665	Sequence 185665, A
c 591	10	52.6	20	6	US-10-668-050-106	Sequence 106, App	c 664	10	52.6	25	8	US-11-217-529-191346	Sequence 191346, A
c 592	10	52.6	20	6	US-10-668-050-107	Sequence 107, App	c 665	10	52.6	25	8	US-11-217-529-191347	Sequence 191347, A
c 593	10	52.6	20	6	US-10-668-050-108	Sequence 108, App	c 666	10	52.6	25	8	US-11-217-529-191349	Sequence 191349, A
c 594	10	52.6	20	6	US-10-668-050-109	Sequence 109, App	c 667	10	52.6	25	9	US-11-348-413-45022	Sequence 45022, A
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c 596	10	52.6	20	7	US-11-247-968A-14	Sequence 14, Appl	c 669	10	52.6	25	9	US-11-348-413-45024	Sequence 45024, A
c 597	10	52.6	20	7	US-11-247-968A-15	Sequence 15, Appl	c 670	10	52.6	25	9	US-11-348-413-45025	Sequence 45025, A
c 598	10	52.6	20	7	US-11-260-845-187	Sequence 187, App	c 671	10	52.6	25	9	US-11-348-413-45026	Sequence 45026, A
c 599	10	52.6	20	7	US-11-260-845-188	Sequence 188, App	c 672	10	52.6	25	9	US-11-348-413-45027	Sequence 45027, A
c 600	10	52.6	20	7	US-11-260-845-189	Sequence 189, App	c 673	10	52.6	25	9	US-11-348-413-70472	Sequence 70472, A
c 601	10	52.6	20	7	US-11-438-172-9	Sequence 9, Appli	c 674	10	52.6	25	9	US-11-348-413-70473	Sequence 70473, A
c 602	10	52.6	20	7	US-11-320-072-242	Sequence 242, App	c 675	10	52.6	25	9	US-11-348-413-70474	Sequence 70474, A
c 603	10	52.6	20	9	US-11-301-360-920	Sequence 920, App	c 676	10	52.6	25	9	US-11-348-413-70475	Sequence 70475, A
c 604	10	52.6	20	9	US-11-301-360-921	Sequence 921, App	c 677	10	52.6	25	9	US-11-348-413-70476	Sequence 70476, A
c 605	10	52.6	20	9	US-11-250-830-21	Sequence 21, Appl	c 678	10	52.6	25	9	US-11-348-413-70477	Sequence 70477, A
c 606	10	52.6	21	6	US-10-511-937-1461	Sequence 1461, Ap	c 679	10	52.6	25	9	US-11-348-413-74574	Sequence 74574, A
c 607	10	52.6	21	7	US-11-260-845-174	Sequence 174, App	c 680	10	52.6	25	9	US-11-348-413-74575	Sequence 74575, A

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741	10	52.6	25	9	US-11-348-413-600032	Sequence 600032,	c 814	10	52.6	25	9	US-10-858-164-802	Sequence 802, App
742	10	52.6	25	9	US-11-348-413-614229	Sequence 614229,	c 815	10	52.6	25	9	US-11-293-024-38	Sequence 38, App
743	10	52.6	25	9	US-11-348-413-614230	Sequence 614230,	c 816	10	52.6	25	9	US-11-293-024-38	Sequence 38, App
744	10	52.6	25	9	US-11-348-413-614231	Sequence 614231,	c 817	10	52.6	25	9	US-11-348-220-24	Sequence 24, App
745	10	52.6	25	9	US-11-348-413-614232	Sequence 614232,	c 818	10	52.6	25	9	US-11-348-013-172	Sequence 172, App
746	10	52.6	25	9	US-11-348-413-614233	Sequence 614233,	c 819	10	52.6	25	9	US-10-858-164-172	Sequence 164, App
747	10	52.6	25	9	US-11-348-413-661492	Sequence 661492,	c 820	10	52.6	25	9	US-11-260-845-170	Sequence 170, App
748	10	52.6	25	9	US-11-348-413-663896	Sequence 663896,	c 821	10	52.6	25	9	US-11-260-845-175	Sequence 175, App
749	10	52.6	25	9	US-11-348-413-696321	Sequence 696321,	c 822	10	52.6	25	9	US-11-260-845-185	Sequence 185, App
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751	10	52.6	25	9	US-11-348-413-711303	Sequence 711303,	c 824	10	52.6	25	9	US-11-293-598-39	Sequence 39, App
752	10	52.6	25	9	US-11-348-413-711304	Sequence 711304,	c 825	10	52.6	25	9	US-11-293-598-39	Sequence 39, App
753	10	52.6	25	9	US-11-348-413-711305	Sequence 711305,	c 826	10	52.6	25	9	US-10-858-013-173	Sequence 173, App
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C 829	10	52.6	30	6	US-10-526-765-61	Sequence 61, Appl	C 902	9.8	51.6	25	8	US-11-217-529-68219	Sequence 68219, A
C 830	10	52.6	30	6	US-10-858-013-176	Sequence 176, Appl	C 903	9.8	51.6	25	8	US-11-217-529-69985	Sequence 69985, A
C 831	10	52.6	30	6	US-10-565-487-10	Sequence 10, Appl	C 904	9.8	51.6	25	8	US-11-217-529-69986	Sequence 69986, A
C 832	10	52.6	30	6	US-10-858-164-176	Sequence 176, App	C 905	9.8	51.6	25	8	US-11-217-529-69997	Sequence 69997, A
C 833	9.8	51.6	15	6	US-10-998-483A-17	Sequence 17, Appl	C 906	9.8	51.6	25	8	US-11-217-529-74234	Sequence 74234, A
C 834	9.8	51.6	17	6	US-10-525-126-14	Sequence 14, Appl	C 907	9.8	51.6	25	8	US-11-217-529-96560	Sequence 96560, A
C 835	9.8	51.6	18	6	US-10-501-834-114	Sequence 114, App	C 908	9.8	51.6	25	8	US-11-217-529-100074	Sequence 100074, A
C 836	9.8	51.6	18	6	US-10-517-441-898	Sequence 898, App	C 909	9.8	51.6	25	8	US-11-217-529-109510	Sequence 109510, A
C 837	9.8	51.6	18	6	US-10-997-763-23	Sequence 23, Appl	C 910	9.8	51.6	25	8	US-11-217-529-115540	Sequence 115540, A
C 838	9.8	51.6	18	7	US-11-299-025-97	Sequence 97, Appl	C 911	9.8	51.6	25	8	US-11-217-529-134252	Sequence 134252, A
C 839	9.8	51.6	18	7	US-11-370-584-5954	Sequence 5954, App	C 912	9.8	51.6	25	8	US-11-217-529-140362	Sequence 140362, A
C 840	9.8	51.6	18	7	US-11-370-584-11203	Sequence 11203, A	C 913	9.8	51.6	25	8	US-11-217-529-147602	Sequence 147602, A
C 841	9.8	51.6	18	7	US-11-370-584-11780	Sequence 11780, A	C 914	9.8	51.6	25	8	US-11-217-529-149864	Sequence 149864, A
C 842	9.8	51.6	18	7	US-11-369-203A-151	Sequence 151, App	C 915	9.8	51.6	25	8	US-11-217-529-155636	Sequence 155636, A
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C 844	9.8	51.6	19	6	US-10-825-485-300	Sequence 300, App	C 917	9.8	51.6	25	8	US-11-217-529-155639	Sequence 155639, A
C 845	9.8	51.6	19	6	US-10-825-485-607	Sequence 607, App	C 918	9.8	51.6	25	8	US-11-217-529-170170	Sequence 170170, A
C 846	9.8	51.6	19	6	US-10-753-718-2096	Sequence 2096, App	C 919	9.8	51.6	25	9	US-11-005-836-60	Sequence 60, Appl
C 847	9.8	51.6	19	6	US-10-753-718-2097	Sequence 2097, App	C 920	9.8	51.6	25	9	US-11-348-413-20659	Sequence 20659, A
C 848	9.8	51.6	19	6	US-10-753-718-2098	Sequence 2098, App	C 921	9.8	51.6	25	9	US-11-348-413-24415	Sequence 24415, A
C 849	9.8	51.6	19	6	US-10-723-683-379	Sequence 379, App	C 922	9.8	51.6	25	9	US-11-348-413-24416	Sequence 24416, A
C 850	9.8	51.6	19	7	US-11-370-584-3963	Sequence 3963, App	C 923	9.8	51.6	25	9	US-11-348-413-63441	Sequence 63441, A
C 851	9.8	51.6	19	7	US-11-370-584-6637	Sequence 6637, App	C 924	9.8	51.6	25	9	US-11-348-413-71713	Sequence 71713, A
C 852	9.8	51.6	19	7	US-11-305-699-4	Sequence 4, Appl	C 925	9.8	51.6	25	9	US-11-348-413-178644	Sequence 178644, A
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C 854	9.8	51.6	19	7	US-11-299-391-1098	Sequence 1098, App	C 927	9.8	51.6	25	9	US-11-348-413-209266	Sequence 209266, A
C 855	9.8	51.6	19	7	US-11-299-391-1422	Sequence 1422, App	C 928	9.8	51.6	25	9	US-11-348-413-209267	Sequence 209267, A
C 856	9.8	51.6	19	9	US-11-217-936-3377	Sequence 3377, App	C 929	9.8	51.6	25	9	US-11-348-413-209268	Sequence 209268, A
C 857	9.8	51.6	19	9	US-11-217-936-3350	Sequence 3350, App	C 930	9.8	51.6	25	9	US-11-348-413-209269	Sequence 209269, A
C 858	9.8	51.6	20	6	US-10-511-937-1310	Sequence 1310, App	C 931	9.8	51.6	25	9	US-11-348-413-231758	Sequence 231758, A
C 859	9.8	51.6	20	6	US-10-511-937-1444	Sequence 1444, App	C 932	9.8	51.6	25	9	US-11-348-413-231759	Sequence 231759, A
C 860	9.8	51.6	20	6	US-10-511-937-1879	Sequence 1879, App	C 933	9.8	51.6	25	9	US-11-348-413-231759	Sequence 231759, A
C 861	9.8	51.6	20	7	US-10-533-878-3	Sequence 3, Appl	C 934	9.8	51.6	25	9	US-11-348-413-237881	Sequence 237881, A
C 862	9.8	51.6	20	7	US-11-370-584-6865	Sequence 6865, App	C 935	9.8	51.6	25	9	US-11-348-413-237882	Sequence 237882, A
C 863	9.8	51.6	20	8	US-11-222-810-8	Sequence 8, Appl	C 936	9.8	51.6	25	9	US-11-348-413-237883	Sequence 237883, A
C 864	9.8	51.6	20	8	US-11-222-810-55	Sequence 55, Appl	C 937	9.8	51.6	25	9	US-11-348-413-237884	Sequence 237884, A
C 865	9.8	51.6	20	8	US-11-200-624-38	Sequence 38, Appl	C 938	9.8	51.6	25	9	US-11-348-413-237885	Sequence 237885, A
C 866	9.8	51.6	20	8	US-11-170-728-10	Sequence 10, Appl	C 939	9.8	51.6	25	9	US-11-348-413-237886	Sequence 237886, A
C 867	9.8	51.6	20	9	US-11-294-621-183	Sequence 183, App	C 940	9.8	51.6	25	9	US-11-348-413-237886	Sequence 237886, A
C 868	9.8	51.6	20	9	US-11-035-114-109	Sequence 109, App	C 941	9.8	51.6	25	9	US-11-348-413-265175	Sequence 265175, A
C 869	9.8	51.6	21	6	US-10-511-937-925	Sequence 925, App	C 942	9.8	51.6	25	9	US-11-348-413-270053	Sequence 270053, A
C 870	9.8	51.6	21	7	US-11-370-584-10436	Sequence 10436, A	C 943	9.8	51.6	25	9	US-11-348-413-270054	Sequence 270054, A
C 871	9.8	51.6	21	7	US-11-370-584-10974	Sequence 10974, A	C 944	9.8	51.6	25	9	US-11-348-413-270055	Sequence 270055, A
C 872	9.8	51.6	21	8	US-11-321-421-194	Sequence 194, App	C 945	9.8	51.6	25	9	US-11-348-413-270056	Sequence 270056, A
C 873	9.8	51.6	21	8	US-11-197-219-48	Sequence 48, Appl	C 946	9.8	51.6	25	9	US-11-348-413-270057	Sequence 270057, A
C 874	9.8	51.6	22	6	US-10-511-937-2383	Sequence 2383, App	C 947	9.8	51.6	25	9	US-11-348-413-270058	Sequence 270058, A
C 875	9.8	51.6	22	6	US-10-524-193A-128	Sequence 128, App	C 948	9.8	51.6	25	9	US-11-348-413-270059	Sequence 270059, A
C 876	9.8	51.6	22	8	US-11-257-502-106	Sequence 106, App	C 949	9.8	51.6	25	9	US-11-348-413-324253	Sequence 324253, A
C 877	9.8	51.6	22	8	US-11-257-502-206	Sequence 206, App	C 950	9.8	51.6	25	9	US-11-348-413-324254	Sequence 324254, A
C 878	9.8	51.6	22	8	US-11-074-497-34	Sequence 34, Appl	C 951	9.8	51.6	25	9	US-11-348-413-354645	Sequence 354645, A
C 879	9.8	51.6	22	9	US-11-298-875A-52	Sequence 52, Appl	C 952	9.8	51.6	25	9	US-11-348-413-354646	Sequence 354646, A
C 880	9.8	51.6	23	6	US-10-844-527D-2	Sequence 2, Appl	C 953	9.8	51.6	25	9	US-11-348-413-354647	Sequence 354647, A
C 881	9.8	51.6	23	7	US-11-340-080-90	Sequence 90, Appl	C 954	9.8	51.6	25	9	US-11-348-413-354648	Sequence 354648, A
C 882	9.8	51.6	23	7	US-11-340-080-91	Sequence 91, Appl	C 955	9.8	51.6	25	9	US-11-348-413-354649	Sequence 354649, A
C 883	9.8	51.6	23	8	US-11-181-115-78	Sequence 78, Appl	C 956	9.8	51.6	25	9	US-11-348-413-354650	Sequence 354650, A
C 884	9.8	51.6	23	8	US-11-078-073-90	Sequence 90, Appl	C 957	9.8	51.6	25	9	US-11-348-413-390675	Sequence 390675, A
C 885	9.8	51.6	23	8	US-11-078-073-91	Sequence 91, Appl	C 958	9.8	51.6	25	9	US-11-348-413-393402	Sequence 393402, A
C 886	9.8	51.6	23	8	US-11-321-421-227	Sequence 227, App	C 959	9.8	51.6	25	9	US-11-348-413-416179	Sequence 416179, A
C 887	9.8	51.6	24	6	US-10-511-937-1531	Sequence 1531, App	C 960	9.8	51.6	25	9	US-11-348-413-416180	Sequence 416180, A
C 888	9.8	51.6	24	6	US-10-520-350-76	Sequence 76, Appl	C 961	9.8	51.6	25	9	US-11-348-413-416181	Sequence 416181, A
C 889	9.8	51.6	24	7	US-11-299-025-636	Sequence 636, App	C 962	9.8	51.6	25	9	US-11-348-413-416383	Sequence 416383, A
C 890	9.8	51.6	24	8	US-11-257-502-103	Sequence 103, App	C 963	9.8	51.6	25	9	US-11-348-413-416384	Sequence 416384, A
C 891	9.8	51.6	25	7	US-11-345-018-5	Sequence 5, Appl	C 964	9.8	51.6	25	9	US-11-348-413-425589	Sequence 425589, A
C 892	9.8	51.6	25	8	US-11-217-529-8165	Sequence 8165, App	C 965	9.8	51.6	25	9	US-11-348-413-425590	Sequence 425590, A
C 893	9.8	51.6	25	8	US-11-217-529-10803	Sequence 10803, A	C 966	9.8	51.6	25	9	US-11-348-413-425591	Sequence 425591, A
C 894	9.8	51.6	25	8	US-11-217-529-11504	Sequence 11504, A	C 967	9.8	51.6	25	9	US-11-348-413-425592	Sequence 425592, A
C 895	9.8	51.6	25	8	US-11-217-529-24367	Sequence 24367, A	C 968	9.8	51.6	25	9	US-11-348-413-425593	Sequence 425593, A
C 896	9.8	51.6	25	8	US-11-217-529-26585	Sequence 26585, A	C 969	9.8	51.6	25	9	US-11-348-413-429017	Sequence 429017, A
C 897	9.8	51.6	25	8	US-11-217-529-38703	Sequence 38703, A	C 970	9.8	51.6	25	9	US-11-348-413-433687	Sequence 433687, A
C 898	9.8	51.6	25	8	US-11-217-529-43822	Sequence 43822, A	C 971	9.8	51.6	25	9	US-11-348-413-433688	Sequence 433688, A
C 899	9.8	51.6	25	8	US-11-217-529-51675	Sequence 51675, A	C 972	9.8	51.6	25	9	US-11-348-413-433689	Sequence 433689, A

; APPLICANT: Charani, Neda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AUTISM
; FILE REFERENCE: UMD0115US.P1
; CURRENT APPLICATION NUMBER: US/11/324,563
; CURRENT FILING DATE: 2006-01-03
; PRIOR APPLICATION NUMBER: PCT/US2004/021301
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US 60/721,192
; PRIOR FILING DATE: 2005-09-28
; PRIOR APPLICATION NUMBER: US 60/484,633
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-11-324-563-66

Query Match 66.3%; Score 12.6; DB 9; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGGTGCT 19
|||||
Db 21 CGAGAAGGGAGGAGGAGTT 3

RESULT 5

US-11-378-920-23/c
; Sequence 23, Application US/11378920
; Publication No. US20060218674A1
; GENERAL INFORMATION:
; APPLICANT: SAKAI, HAJIME
; APPLICANT: NAGASAWA, NORUHIRO
; TITLE OF INVENTION: ALTERATION OF PLANT EMBRYO/ENDOSPERM SIZE DURING DEVELOPMENT
; FILE REFERENCE: B01536 US NA
; CURRENT APPLICATION NUMBER: US/11/378,920
; CURRENT FILING DATE: 2006-03-17
; PRIOR APPLICATION NUMBER: 60/664,512
; PRIOR FILING DATE: 2005-03-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer LOB F2
US-11-378-920-23

Query Match 66.3%; Score 12.6; DB 7; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGAAGGGGGTGGGTGCT 19
|||||
Db 23 CGAGAAGTGGTGGGAGCT 5

RESULT 6

US-10-511-937-1926
; Sequence 1926, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1926
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: 1926
US-10-511-937-1926

Query Match 64.2%; Score 12.2; DB 6; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGGTGCT 19
|||||
Db 1 AGAAGGTGGTGGCTGT 17

RESULT 7

US-10-548-681-35/c
; Sequence 35, Application US/10548681
; Publication No. US20060166214A1
; GENERAL INFORMATION:
; APPLICANT: Yukio KATO
; APPLICANT: Koichiro TSUJI
; APPLICANT: Chika KOIKE
; TITLE OF INVENTION: Marker for detecting mesenchymal stem cell and method of distinguishing
; FILE REFERENCE: 4439-4035
; CURRENT APPLICATION NUMBER: US/10/548,681
; CURRENT FILING DATE: 2005-09-08
; PRIOR APPLICATION NUMBER: JP2003-63077
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MHC Class 2 DR beta3 antisense primer
US-10-548-681-35

Query Match 64.2%; Score 12.2; DB 6; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAGAAGGGGGTGGGTGC 18
|||||
Db 18 GAGAACGTGGTGTGTC 2

RESULT 8

US-11-217-529-60224/c
; Sequence 60224, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-60224

Query Match 64.2%; Score 12.2; DB 8; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGTGCT 19
||||| ||||| ||||| ||
DB 25 AGAAGAGGGTTGGTCT 9

RESULT 9
US-11-348-413-1052286
; Sequence 1052286, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 57; Stop 81;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052286

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGTGCT 19
||||| ||||| ||||| ||
DB 9 AAAATGGGTGGTGCT 25

RESULT 10
US-11-348-413-1052287
; Sequence 1052287, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052287
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 58; Stop 82;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052287

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGTGCT 19
||||| ||||| ||||| ||
DB 8 AAAATGGGTGGTGCT 24

RESULT 11
US-11-348-413-1052288
; Sequence 1052288, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 59; Stop 83;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052288

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 7 AAAATGGTGGGTGCT 23

RESULT 12

US-11-348-413-1052289
; Sequence 1052289, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052289
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 60; Stop 84;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052289

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 6 AAAATGGTGGGTGCT 22

RESULT 13

US-11-348-413-1052290
; Sequence 1052290, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 65; Stop 89;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052290

Query Match 64.2%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGAAGGGGTGGTGCT 19
Db 1 AAAATGGTGGGTGCT 17

RESULT 14

US-11-199-903-3
; Sequence 3, Application US/11199903
; Publication No. US20060216274A1
; GENERAL INFORMATION:
; APPLICANT: Kurtzman, Gary J.
; APPLICANT: Engelman, Edgar G.
; APPLICANT: Podaskoff, Greg M.
; TITLE OF INVENTION: Induction Of Immune Response To Antigens Expressed By
; TITLE OF INVENTION: Recombinant Adeno-Associated Virus
; FILE REFERENCE: AVIGEN-03398
; CURRENT APPLICATION NUMBER: US/11/199,903
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US/09/858,728
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/121,162
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: 60/053,773
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-199-903-3

Query Match 62.1%; Score 11.8; DB 7; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAAGGGGTGGG 15
Db 1 GGGAAGGGGTGGG 15

RESULT 15

US-11-305-629-9
; Sequence 9, Application US/11305629
; Publication No. US20060099185A1
; GENERAL INFORMATION:
; APPLICANT: PODSAKOFF, GREGORY M.
; APPLICANT: KURTZMAN, GARY J.
; TITLE OF INVENTION: METHODS OF TREATING ANEMIA USING
; RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/305,629
FILING DATE: 15-Dec-2005
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/458,857
FILING DATE: 10-Jun-2003
APPLICATION NUMBER: US/08/785,750
FILING DATE: 16-Jan-1997
APPLICATION NUMBER: US 08/588,355
FILING DATE: 18-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: MCCracken, Thomas P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 0800-0009.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 325-7812
TELEFAX: (415) 325-7823

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-11-305-629-9
Query Match 62.1%; Score 11.8; DB 8; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAAGGGGGTGGG 15
DB 1 GGGAAGGGGGTGGG 15

RESULT 16

Sequence 11, Application US/11329941
Publication No. US20060104954A1
GENERAL INFORMATION:
APPLICANT: Podsakoff, Gregory
APPLICANT: Watson, Gordon
APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
TREATMENT OF LYSSOMAL DISORDERS
FILE REFERENCE: 0800-0021
CURRENT APPLICATION NUMBER: US/11/329,941
CURRENT FILING DATE: 2006-01-11
PRIOR APPLICATION NUMBER: US/10/421,175
PRIOR FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: US/09/715,858
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer

US-11-329-941-11
Query Match 62.1%; Score 11.8; DB 8; Length 21;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGAAGGGGGTGGG 15

Db 1 GGGAAGGGGGTGGG 15

RESULT 17

US-11-348-413-635553
Sequence 635553, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 635553
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe
NAME/KEY: misc feature
LOCATION: (1)-(25)
OTHER INFORMATION: SEQ ID NO: 806; WAN01UJOT_at; Start 593; Stop 617;
OTHER INFORMATION: 0111010000000000
US-11-348-413-635553

Query Match 62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGTG 17
DB 4 AGAAGGGGGTGGATG 18

RESULT 18

US-11-348-413-709656/c
Sequence 709656, Application US/11348413
Publication No. US20060160121A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Murphy, Ellen
APPLICANT: Olmsted, Stephen
TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
FILE REFERENCE: 031896-084100 (AM 101724)
CURRENT APPLICATION NUMBER: US/11/348,413
CURRENT FILING DATE: 2006-02-07
PRIOR APPLICATION NUMBER: PCT/US05/035471
PRIOR FILING DATE: 2005-10-05
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 11/243,445
PRIOR FILING DATE: 2005-10-05
PRIOR APPLICATION NUMBER: US 60/615,573
PRIOR FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 1276209
SEQ ID NO 709656
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: probe

```
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 2889; WAN01UNF9_at; Start 82; Stop 106;
; OTHER INFORMATION: 11111100000000
US-11-348-413-709656

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
DB      19 AAGGGGGTGGGTGCT 5

RESULT 19
US-11-348-413-1052291
; Sequence 1052291, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052291
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 66; Stop 90;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052291

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
DB      2 AATGGTGTGGGTGCT 16

RESULT 20
US-11-348-413-1052292
; Sequence 1052292, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
```

```
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1052292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 12492; WAN01UOMA_at; Start 67; Stop 91;
; OTHER INFORMATION: 00000000011101
US-11-348-413-1052292

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
DB      1 AATGGTGTGGGTGCT 15

RESULT 21
US-11-348-413-1236138
; Sequence 1236138, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1236138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 17507; WAN01UQWB_at; Start 138; Stop 162;
; OTHER INFORMATION: 000000000000001
US-11-348-413-1236138

Query Match      62.1%; Score 11.8; DB 9; Length 25;
Best Local Similarity 86.7%; Pred. No. 2.8e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 AAGGGGGTGGGTGCT 19
DB      8 AAAGGTGTGGGTGCT 22

RESULT 22
US-11-529-89292
; Sequence 89292, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 89292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-89292
```

```
Query Match          61.1%; Score 11.6; DB 8; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2  GAGAAAGGGGTGGGTGCT 19
|||||  |||||  |||||  |||||
Db      1  GAGAAATCCGGTGGTGTCT 18
```

```
RESULT 23
US-11-348-413-69158
; Sequence 69158, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 69158
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4; Start 584; Stop 608;
; OTHER INFORMATION: 00100000000000
US-11-348-413-69158
```

```
Query Match          61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2  GAGAAAGGGGTGGGTGCT 19
|||||  |||||  |||||  |||||
Db      1  GAGAAAGAGGAAGTGTCT 18
```

```
RESULT 24
US-11-348-413-480499
```

```
; Sequence 480499, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQEO; Start 146; Stop 170;
; OTHER INFORMATION: 000000000001000
US-11-348-413-480499
```

```
Query Match          61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2  GAGAAAGGGGTGGGTGCT 19
|||||  |||||  |||||  |||||
Db      8  GATAATGGGATGGTGTCT 25
```

```
RESULT 25
US-11-348-413-480500
; Sequence 480500, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480500
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQEO; Start 147; Stop 171;
; OTHER INFORMATION: 000000000001000
US-11-348-413-480500
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGTGCT 19
Db 7 GATAATGGGATGGTGCT 24

RESULT 26
US-11-348-413-480501
; Sequence 480501, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 480501
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14366; WAN01UQBO; Start 148; Stop 172;
; OTHER INFORMATION: 00000000001000
US-11-348-413-480501

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGTGCT 19
Db 6 GATAATGGGATGGTGCT 23

RESULT 27
US-11-348-413-649751
; Sequence 649751, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 649751
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4_at; Start 583; Stop 607;
; OTHER INFORMATION: 0010000000000000
US-11-348-413-660009

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGTGCT 19
Db 2 GAGAAAGGAGGAGGTGCT 19

RESULT 29
US-11-348-413-783470/c
; Sequence 783470, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1189; WAN01UK4Y_at; Start 177; Stop 201;
; OTHER INFORMATION: 0000100000000000
US-11-348-413-649751

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGTGCT 19
Db 3 GAGAAAGGCGGAGGTACT 20

RESULT 28
US-11-348-413-660009
; Sequence 660009, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 660009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 1472; WAN01UKK4_at; Start 583; Stop 607;
; OTHER INFORMATION: 0010000000000000
US-11-348-413-660009

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAGAGGGGGTGGTGCT 19
Db 2 GAGAAAGGAGGAGGTGCT 19

RESULT 29
US-11-348-413-783470/c
; Sequence 783470, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
```

```
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783470
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAO_at; Start 112; Stop 136;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783470
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 23 GAGAGGGTGGTGGCTGT 6
```

```
RESULT 30
US-11-348-413-783471/c
; Sequence 783471, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783471
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAO_at; Start 115; Stop 139;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783471
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 20 GAGAGGGTGGTGGCTGT 3
```

RESULT 31

```
US-11-348-413-783472/c
; Sequence 783472, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 783472
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 5091; WAN01PAAO_at; Start 117; Stop 141;
; OTHER INFORMATION: 000001000000000
US-11-348-413-783472
```

```
Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 GAGAGGGGGTGGTGCT 19
    ||||| ||| ||| |||
Db 18 GAGAGGGTGGTGGCTGT 1
```

RESULT 32

```
US-11-348-413-1225381
; Sequence 1225381, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 1225381
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 17229; WAN01UQN2_at; Start 349; Stop 373;
; OTHER INFORMATION: 0000000000001100
```

US-11-348-413-1225381

Query Match 61.1%; Score 11.6; DB 9; Length 25;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 1 GACAACGGGTGAGTGCT 18

RESULT 33
US-11-260-845-310/c
; Sequence 310, Application US/11260845
; Publication No. US20060183207A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamicheva, Natasha
; TITLE OF INVENTION: FEN Endonucleases
; FILE REFERENCE: FORS-09451
; CURRENT APPLICATION NUMBER: US/11/260,845
; CURRENT FILING DATE: 2005-11-27
; NUMBER OF SEQ ID NOS: 410
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 310
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Archaeoglobus veneficus
US-11-260-845-310

Query Match 61.1%; Score 11.6; DB 7; Length 27;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGAGAGGGGGTGGTGTC 18
DB 22 GGAGAAGTGGATCGTGTC 5

RESULT 34
US-11-368-233-179/c
; Sequence 179, Application US/11368233
; Publication No. US20060205040A1
; GENERAL INFORMATION:
; APPLICANT: Sampath, Rangarajan
; TITLE OF INVENTION: COMPOSITIONS FOR USE IN IDENTIFICATION OF ADVENTITIOUS VIRUSES
; FILE REFERENCE: DIBIS-0085US1 (10774)
; CURRENT APPLICATION NUMBER: US/11/368,233
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: 60/658,248
; PRIOR FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: 60/705,631
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/732,539
; PRIOR FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/740,617
; PRIOR FILING DATE: 2005-11-28
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-368-233-179

Query Match 61.1%; Score 11.6; DB 7; Length 28;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19

DB 26 GAGAATGGGTGGGCCT 9

RESULT 35
US-11-368-233-180/c
; Sequence 180, Application US/11368233
; Publication No. US20060205040A1
; GENERAL INFORMATION:
; APPLICANT: Sampath, Rangarajan
; TITLE OF INVENTION: COMPOSITIONS FOR USE IN IDENTIFICATION OF ADVENTITIOUS VIRUSES
; FILE REFERENCE: DIBIS-0085US1 (10774)
; CURRENT APPLICATION NUMBER: US/11/368,233
; CURRENT FILING DATE: 2006-03-03
; PRIOR APPLICATION NUMBER: 60/658,248
; PRIOR FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: 60/705,631
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/732,539
; PRIOR FILING DATE: 2005-11-01
; PRIOR APPLICATION NUMBER: 60/740,617
; PRIOR FILING DATE: 2005-11-28
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (24)...(24)
; OTHER INFORMATION: I
US-11-368-233-180

Query Match 61.1%; Score 11.6; DB 7; Length 28;
Best Local Similarity 77.8%; Pred. No. 3.5e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAGAGGGGGTGGTGCT 19
DB 26 GAGAATGGGTGGGCCT 9

RESULT 36
US-11-217-936-4208/c
; Sequence 4208, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4208
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-4208

Query Match 60.0%; Score 11.4; DB 9; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 6 AGGGGGTGGTGC 18
Db 18 AGGGGGTGGTGC 6

RESULT 37
US-11-217-936-4466
; Sequence 4466, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (siRNA)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4466
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-4466

Query Match 60.0%; Score 11.4; DB 9; Length 19;
Best Local Similarity 76.9%; Pred. No. 4.1e+04;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGGGGGTGGTGC 18
Db 2 AGGGGGUUGUGC 14

RESULT 38
US-11-316-132-25
; Sequence 25, Application US/11316132
; Publication No. US20060100153A1
; GENERAL INFORMATION:
; APPLICANT: Shridhar, Viji
; APPLICANT: Roberts, Lewis R.
; APPLICANT: Kaufmann, Scott H.
; TITLE OF INVENTION: Hsulf-1 Nucleic Acids, Polypeptides and
; TITLE OF INVENTION: Methods of Using
; FILE REFERENCE: 07039/449001
; CURRENT APPLICATION NUMBER: US/11/316,132
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/778,607
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/446,945
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-316-132-25

Query Match 60.0%; Score 11.4; DB 8; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.1e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AGGGGGTGGTGC 18
Db 2 AGAGGGTGGTGC 14
```

```
RESULT 39
US-10-818-956-78/c
; Sequence 78, Application US/10818956
; Publication No. US20060134639A1
; GENERAL INFORMATION:
; APPLICANT: Van Huffel, Christophe
; APPLICANT: Remacle, Jose
; APPLICANT: Bulow, Sven
; APPLICANT: Zammattéo, Nathalie
; TITLE OF INVENTION: METHOD FOR THE DETERMINATION OF CELLULAR
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION
; FILE REFERENCE: KLAUS2.006AUS
; CURRENT APPLICATION NUMBER: US/10/818,956
; CURRENT FILING DATE: 2004-04-06
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-818-956-78

Query Match 60.0%; Score 11.4; DB 6; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTG 13
Db 15 GGAGAGGTGGTG 3

RESULT 40
US-11-317-660-380/c
; Sequence 380, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-RHOADES, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; TITLE OF INVENTION: AND FOR ALTERING MIRNA AND TARGET EXPRESSION
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIOR APPLICATION NUMBER: 60/639,231
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 380
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-317-660-380

Query Match 60.0%; Score 11.4; DB 7; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGAGGGGGTG 13
Db 15 GGAGAGGTGGTG 3

RESULT 41
US-11-317-660-1139
; Sequence 1139, Application US/11317660
; Publication No. US20060185027A1
; GENERAL INFORMATION:
```



```
; APPLICANT: BARTEL, DAVID P.
; APPLICANT: JONES-BROADBENT, MATTHEW W.
; APPLICANT: LEWIS, BENJAMIN P.
; APPLICANT: BURGE, CHRISTOPHER B.
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR IDENTIFYING MIRNA TARGETS
; FILE REFERENCE: W0571.70013US01
; CURRENT APPLICATION NUMBER: US/11/317,660
; CURRENT FILING DATE: 2005-12-23
; PRIOR FILING DATE: 2004-12-23
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1139
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-11-317-660-1139

Query Match          60.0%; Score 11.4; DB 7; Length 22;
Best Local Similarity 84.6%; Pred. No. 4.2e+04;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGGGGTG 13
    ||||| |||
Db 8 GGAGGAAGGGGGUG 20

RESULT 42
US-11-242-139-94/c
; Sequence 94, Application US/11242139
; Publication No. US20060099619A1
; GENERAL INFORMATION:
; APPLICANT: REMACLE, JOSE
; APPLICANT: DU LONGUEVILLE, FRANCOISE
; APPLICANT: HAMELS, SANDRINE
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MIRNA ON MICRO-ARRAYS
; FILE REFERENCE: 035642-0107
; CURRENT APPLICATION NUMBER: US/11/242,139
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 10/637,656
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-242-139-94

Query Match          60.0%; Score 11.4; DB 8; Length 22;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAGGAAGGGGGTG 13
    ||||| |||
Db 15 GGAGGAAGGGGGTG 3

RESULT 43
US-11-283-550-1462/c
; Sequence 1462, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
```

```
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1462
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1462

Query Match          60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
    ||||| |||
Db 23 AGAAGGGGGTGGG 11

RESULT 44
US-11-283-550-1463/c
; Sequence 1463, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1463
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1463

Query Match          60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
    ||||| |||
Db 22 AGAAGGGGGTGGG 10

RESULT 45
US-11-283-550-1464/c
; Sequence 1464, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
```

; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1464
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1464

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 21 AGAAGGGGGTGGG 9

RESULT 46
US-11-283-550-1465/c
; Sequence 1465, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1465
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1465

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 20 AGAAGGGGGTGGG 8

RESULT 47

US-11-283-550-1466/c
; Sequence 1466, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1466

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15
|||||
Db 19 AGAAGGGGGTGGG 7

RESULT 48
US-11-283-550-1467/c
; Sequence 1467, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biotherapeutics, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1467

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGAAGGGGGTGGG 15

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
Db 16 AGAAGGGGGTGGG 4

Search completed: October 14, 2006, 20:26:48
Job time : 133 secs

Db 18 AGAAGGGGGTGGG 6
|||||

RESULT 49
US-11-283-550-1468/c
; Sequence 1468, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biopharmaceuticals, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1468
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1468

Query Match 60.0%; Score 11.4; DB 8; Length 23;
Best Local Similarity 92.3%; Pred. No. 4.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AGAAGGGGGTGGG 15
Db 17 AGAAGGGGGTGGG 5
|||||

RESULT 50
US-11-283-550-1469/c
; Sequence 1469, Application US/11283550
; Publication No. US20060134189A1
; GENERAL INFORMATION:
; APPLICANT: MacLachlan, Ian
; APPLICANT: Jeffs, Lloyd B.
; APPLICANT: Judge, Adam
; APPLICANT: Lee, Amy C. H.
; APPLICANT: Palmer, Lorne R.
; APPLICANT: Sood, Vandana
; APPLICANT: Protiva Biopharmaceuticals, Inc.
; TITLE OF INVENTION: siRNA Silencing of Apolipoprotein B
; FILE REFERENCE: 020801-002820US
; CURRENT APPLICATION NUMBER: US/11/283,550
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 60/629,808
; PRIOR FILING DATE: 2004-11-17
; PRIOR APPLICATION NUMBER: US 60/703,226
; PRIOR FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 14212
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1469
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human ApoB siRNA sequence
US-11-283-550-1469

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